From:	Collins, Cynthia
Sent:	Friday, July 19, 2002 3:13 PM
To:	STIC-Biotech/ChemLib
Subject:	sequence search request SN 09/821839

Please search, **both** prior art and interference, for SN 09/821839:

     1) SEQ ID NO:1
     2) SEQ ID NO:2

Thank You,

Cynthia Collins
Art Unit 1638
CM1, 9A12 (office) or 9E12 (mailbox)
(703) 605-1210

3/29/01
PROV. 3/31/00

TYPE OF SEARCH:

Searcher: __~~Point of Contact~~__	NA Sequences: _____	**VENDOR/COST (where applic.)**	
Phone: ____~~P. Sheppard~~____	AA Sequences: _____	STN: _____	
Location~~Telephone number: (703) 308-4499~~	Structures: _____	DIALOG: _____	
Date Picked Up: _____	Bibliographic: _____	Questel/Orbit: _____	
Date Completed: *8/31/02*	Litigation: _____	DRLink: _____	
Searcher Prep/Review: _____	Full text: _____	Lexis/Nexis: _____	
Clerical: _____	Patent Family: _____	Sequence Sys.: _____	
Online time: _____	Other: _____	WWW/Internet: _____	
		Other (specify): _____	

OM protein - protein search, using sw model

GenCore version 4.5
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Run on: July 23, 2002, 14:21:21 ; Search time 34.23 Seconds
                   (without alignments)
                   2921.153 Million cell updates/sec

Title: US-09-821-839-2
Perfect score: 2952
Sequence: 1 MKEIAMRNSKRKPEPTPFAG.........RTTDNELPECVKSLDWLLGQ 578

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 562222

Post-processing: Minimum Match 0%
                   Maximum Match 100%

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   [handwritten]
                   Listing first 45 summaries

1: sp_archaea:*
2: sp_bacteria:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rvirus:*
17: sp_bacteriap:*
...: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match Length	DB	ID	Description
1	2858	96.8	648	10	Q9LQV6	Q9lqv6 arabidopsis
2	281.5	9.5	429	10	081794	081794 arabidopsis
3	263.5	8.9	429	10	Q39070	Q39070 arabidopsis
4	252	8.5	443	10	Q39071	Q39071 arabidopsis
5	251	8.5	434	10	Q9XGI1	Q9xgi1 lycopersico
6	250	8.5	428	10	Q4O337	medicago sa
7	249.5	8.5	444	10	Q9ZUO9	Q9zuo9 arabidopsis
8	246	8.3	458	5	O15996	O15996 hemicentrot
9	243.5	8.2	429	10	Q39068	Q39068 arabidopsis
10	243	8.2	445	10	P90681	P90681 asterina pe
11	242.5	8.2	452	10	024073	024073 medicago sa
12	241	8.2	424	10	Q41731	Q41731 zea mays (m
13	239.5	8.1	429	10	Q9SHP1	Q9shp1 arabidopsis
14	239	8.1	462	5	062573	062573 sphaerechin
15	239	8.1	457	5	Q9NIP5	Q9nip5 strongyloce
16	236.5	8.0	454	10	082717	082717 lupinus lut
17	235.5	8.0	484	10	Q9XGI0	Q9xgi0 medicago sa
18	234.5	7.9	445	10	Q9FG02	Q9fg02 arabidopsis
19	234.5	7.9	445	10	Q39067	Q39067 arabidopsis
20	233.5	7.9	427	10	Q9CAX5	Q9cax5 arabidopsis
21	233	7.9	460	10	Q9LDM4	Q9ldm4 arabidopsis
22	232.5	7.9	446	10	O04398	004398 nicotiana t
23	229.5	7.8	452	10	Q9S957	Q9s957 medicago fa
24	229	7.8	452	10	049959	049959 lupinus lut
25	229	7.8	420	10	Q9XGI5	Q9xgi5 lycopersico
26	228.5	7.7	475	10	Q9SS25	Q9ss25 oryza sativ
27	228	7.7	454	10	Q9XGI4	Q9xgi4 lycopersico
28	227.5	7.7	456	10	Q9FVX0	Q9fvx0 arabidopsis
29	227	7.7	459	10	Q41732	Q41732 zea mays (m
30	225	7.6	502	10	082718	082718 lupinus lut
31	223	7.6	418	10	Q43693	Q43693 arabidopsis
32	222.5	7.5	473	10	Q9SFW6	Q9sfw6 arabidopsis
33	222	7.5	378	10	Q40516	Q40516 nicotiana t
34	220.5	7.5	324	5	Q9XGI3	Q9xgi3 lycopersico
35	219.5	7.4	470	10	O97478	097478 paramecium
36	219.5	7.4	480	10	Q1G64	Q1g64 oryza sativ
37	219.5	7.4	483	10	Q1964	Q1964 nicotiana t
38	219.5	7.4	480	10	Q41M7	Q41m7 medicago sa
39	219	7.4	388	5	O94739	094739 sphaerechin
40	218.5	7.4	470	10	O40514	040514 nicotiana t
41	216.5	7.3	394	13	O98K7	098k7 rana dybows
42	216	7.3	436	10	Q39073	Q39073 arabidopsis
43	215.5	7.3	419	5	O77212	077212 dreissena p
44	215	7.3	417	5	Q94740	Q94740 sphaerechin
45	215	7.3	443	10	Q40794	Q40794 petroseliun

RESULT 1

Q9LQV6   PRELIMINARY;   PRT;   648 AA.

ID   Q9LQV6;
AC   Q9LQV6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   F10B6.15.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M.,
RA   Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,
RA   Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S.,
RA   Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G.,
RA   Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;
RT   "Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
RT   I.";
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Ecker J.R.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Ecker J.R.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]

ALIGNMENTS

RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC006917; AAF79244.1; -.
HSSP; P30274; 1VIN.
DR InterPro; IPR004366; Cyclin.
SMART; SM00385; CYCLIN; 2.
SQ SEQUENCE 648 AA; 73432 MW; 3CB4D8CA66B7EFE CRC64;

Query Match 96.8%; Score 2858; DB 10; Length 648;
Best Local Similarity 94.3%; Pred. No. 4.7e-182;
Matches 565; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

Qy   6 MRNSKRKPEPTPFPAGKKLRSTRLRRKRAQISPVLVQSPLWSKQIGVSAASVDSCSDLLAD 65
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRNSKRKPEPTPFPAGKKLRSTRLRRKRAQISPVLVQSPLWSKQIGVSAASVDSCSDLLAD 60

Qy   66 DNVSCGSSRVEKSSNPKKTLIEEVEVSKPGYNVKETIGDSKFRRITRSYSKLHKEKEGDE 125
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DNVSCGSSRVEKSSNPKKTLIEEVEVSKPGYNVKETIGDSKFRRITRSYSKLHKEKEGDE 120

Qy 126 IEVSESSCVDSNSGAGLRRLNVKGNKINDNDEISFSRSDVTFAGHVSNSRSLNFESENKE 185
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 IEVSESSCVDSNSGAGLRRLNVKGNKINDNDEISFSRSDVTFAGHVSNSRSLNFESENKE 180

Qy 186 SDVVSVISGVEYCSKFGSVTGGADNEEIEISKPSSFVEADSSLGSAKELKPELEIVGCVS 245
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 SDVVSVISGVEYCSKFGSVTGGADNEEIEISKPSSFVEADSSLGSAKELKPELEIVGCVS 240

Qy 246 DLACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGSEFSEKSSSDSP 305
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 DLACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGSEFSEKSSSDSP 300

Qy 306 ISHSRSLYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRFDDEEVEESYLRLRERERSHAY 365
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 ISHSRSLYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRFDDEEVEESYLRLRERERSHAY 360

Qy 366 MRDCAKAYCSRMDNTGLIPRLRSIMYQWIVK---------------------------- 396
         |||||||||||||||||||||||||||||
Db 361 MRDCAKAYCSRMDNTGLIPRLRSIMYQWIVKPKEIYSLLWNLLRFMYQSAMIFFVADCLL 420

Qy 397 ------QCSDMGLLQQETLFLGVGLLLDRFLSKGSFEKSERTLILVGIASLTLATRIEEN 451
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 PDYKQQCSDMGLLQQETLFLGVGLLLDRFLSKGSFEKSERTLILVGIASLTLATRIEENQPYN 480

Qy 452 SIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFENFLWFYLKAARANPEVERKA 511
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 SIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFENFLWFYLKAARANPEVERKA 540

Qy 512 KSLAVTSLSDQTOLCFWPSTVAAALVVLACIEHNKISAYORVIKVHVRTTDNELPECVK 570
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 KSLAVTSLSDQTOLCFWPSTVAAALVVLACIEHNKISAYORVIKVHVRTTDNELPECVK 599

RN [2]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AL031135; CAA20032.1; -.
DR EMBL; AL161587; CAB80278.1; -.
HSSP; P30274; 1VIN.
DR InterPro; IPR004366; Cyclin.
Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 429 AA; 49786 MW; 5BDE8D7171A2FE09 CRC64;

Query Match 9.5%; Score 281.5; DB 10; Length 429;
Best Local Similarity 27.3%; Pred. No. 6.9e-11;
Matches 94; Conservative 69; Mismatches 134; Indels 47; Gaps 13;

Qy 248 ACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGSEFSEKSSSDSPIS 307
         :||:| ||||||||||||||||:|:|:| :|:|:||||||||||| |||||| ||
Db   72 SCDKKKLDSLHPSI-SRSQEETKKLRKPSGNERG---DCIFIDEEEEKNEEVTLDQPMP 125

Qy 308 HS-RSLYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRFDDEEVEESYLRLRERERSHA-- 364
         || | ||||||||||||||||||||||||||||||||||||||||||||||:||:
Db 126 MSLEEPYIEF---------------DPMEEEVEMEDM--EEEQEEPVLDIDEYDANNSLA 168

Qy 365 --YMRDCAKAY----------CSRMD----NTGLIPRLRSIMYQWIVKQCSDMGLLQQETLFL 410
           :||||||| ::|:| ||||||||||||||||:|: |:|||||||||
Db 169 AVEVYQDLYDFYRKTERFSCVPLDYMAQFDISDKMRAILIDWLIEVHDKFELMNETLFL 228

Qy 411 GVGLLLDRFLSKGSFEKSERTLILVGIASLTLATRIEE-NQPYNSIRKRNFTIQNLRYSRHE 469
         ||:||||||||||||||||||||||||:||||||:|:| |:||:||:::| ||||||:
Db 229 TVNLIDRFLSKQAV-ARKKLQLVGLVALILACKYEEVSVP---IVEDLVVISDKAYTRTD 284

Qy 470 VVAMEWLVQEVLNFKCFTPTIFENFLWFYLKAARANPEVERKAKSLAVTSLSDQTOLCFWP 529
         ||||:||||||||||||||:||:::||||||||||::::|:||:::|||:|:|||:|:|||
Db 285 VLEMEKIMLSTLQFNMSLPTCYPLFLKRFLKAAQSDKKLEILASFLIELALVYDEYMRYPP 344

Qy 530 STVAAALVVLA-CIEHNKISAYORVIKVHVRTTDNELPECVKVKSL 572
         || ||:| :|| :|::| : ::| |:|:: :|:||:|:||||:
Db 345 SLLAATAVVTAQCTIHG-FSEWNSTCEFHCHYSENQLLECCRRM 387

RESULT 4

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ID   Q39071      PRELIMINARY;   PRT;   443 AA.
AC   Q39071;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CYCLIN 3A.
GN   CYC3A.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95062258; PubMed=7972055;
RA   Ferreira P.C.G., Hemerly A.S., De Almeida Engler J., Bergounioux C.,
RA   Burssens S., Van Montagu M., Engler G., Inze D.;
RT   "Three discrete classes of Arabidopsis cyclins are expressed during
RT   different intervals of the cell cycle.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:11313-11317(1994).
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR   EMBL; Z31589; CAA83460.1; -.
DR   HSSP; P30274; 1IVIN.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR004367; Cyclin_C.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cell cycle; Cell division; Cyclin.
SQ   SEQUENCE   429 AA;  49768 MW;  46746BB371A2406E CRC64;

Query Match             8.9%;  Score 263.5;  DB 10;  Length 429;
Best Local Similarity  27.1%;  Pred. No. 1.1e-09;
Matches   92;  Conservative   67;  Mismatches  133;  Indels   47;  Gaps  13;

Qy  248 ACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSPSIFFDSGSEFSEKSSSSDSPIS 307
         :|::|||||||||: :|: :|||||||: ||:|||||| |::|: |||||||:|::
Db   72 SCDKKLDSLHPSI-SRSQEETKLKPSSGNEFG-----DCIFIDEEEKNEEVTLDQPMP 125

Qy  308 HS-RSLYLQFKEQFCRSTIPNDFGSSCEEEHIHSELLRFDDEEVEESYLRLRERERSHA-- 364
Db  126 MSLEEPYIEF----------DPMEEEVEMEDM----EEQEEPVLDIGYDANNSLA 168

Qy  365 --YMRDCAKAY-------CSRMD----NTGLIPRLRSIMVQWIVKQCSDMGLQOQETLFL 410
Db  169 AVEYVQDLYDFYRKTERFSCVPLDYMAQQFDISDKMRAILIDWLIEVHDKFELMNETLFL 228

Qy  411 GVGLLDRFLSKGSFKSERTLLIVGIASLTLATRIEE-NOPYNSIRKRNFTIONLRYSRHE 469
Db  229 TVNLIDRFLSKQAV-ARKKLQLVGLVALLLACKYEESVP---IVEDLVVISDKAYTRTD 284

Qy  470 VVAMEWLVQEVLNFKCFTPTFINFLWFYLKAARANPEVERKAKSLAVTSLSDQTQLCFWP 529
Db  285 VLEMEKIMLSTLQFNMSLPTQYFLKRFIKAAQSDKKLEILASFLIELALVDYEMVRYPP 344

Qy  530 STVAAALVVLA-CIEHNKISAYQRVIKVHVRTDNELPE 567
Db  345 SLIAATAVVTAQCTIHG-FSEWNSTCEFHCHYSENQLLE 382
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RESULT 5

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ID   Q9XGI1      PRELIMINARY;   PRT;   434 AA.
AC   Q9XGI1;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CYCLIN B2.
GN   CYCB2.
OS   Lycopersicon esculentum (Tomato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX   NCBI_TaxID=4081;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. WEST VIRGINIA 106; TISSUE=FRUIT;
RX   MEDLINE=20441870; PubMed=10987563;
RA   Joubes J., Walsh D., Raymond P., Chevalier C.;
RT   "Molecular characterization of the expression of distinct classes of
RT   cyclins during the early development of tomato fruit.";
RL   Planta 211:430-439(2000).
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR   EMBL; AJ243455; CAB46645.1; -.
DR   HSSP; P30274; 1IVIN.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR004367; Cyclin_C.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cell cycle; Cell division; Cyclin.
SQ   SEQUENCE   443 AA;  50368 MW;  6F87959899924C71B CRC64;

Query Match             8.5%;  Score 252;  DB 10;  Length 443;
Best Local Similarity  25.4%;  Pred. No. 6.6e-09;
Matches  117;  Conservative   70;  Mismatches  151;  Indels  122;  Gaps  20;

Qy   99 KETIGDSKEFR-----RITRSYSKLHKEKEGDEIEVSESSCVDSNSGAGIRRLNVKGKRIND 154
Db   13 KEAISTSKIRDNNVRVTRSRAK------ALGVSNSPSKPAPKHE-TKRVARPSNKRMA 63

Qy  155 NDEISFSRSDVTFAGHVSNSRS---LNFESENKESDVVSVISGVEYCSKFGSVTGGADNE 211
Db   64 SDNIT----VCNQKRRAVLKDVTNTLAESIISTEGNVRQACK---RGGKETK 108

Qy  212 EIEISKPSSFVEADSSLSGSASAKELKPELEIVGCVSDLACSEKFSEEVSDSLDDESSEQRSE 271
Db  109 QIE--EDGLVDVD--GEKSKLAEDLSKIRMVESLDAS-----ASKELVDCAEEDRS- 155

Qy  272 IYSQYSDFDYSPSIFFDSGSEFSEKSSSSDSPISHSRSLYLQFKEQFCRSTIPNDEGS 331
Db  156 ------DVTDCVQIVDLDSGVQ---------------SLYAA 181

Qy  332 SCEEEIH-SELLRFDDEEVEESYLRLRERERSHAYM---RDCAKAYCSRMDNTGLIPRL 386
Db  182 SIYDSINVAEL---------EQRPSTSYMVQLRD---------IDPTM 212

Qy  387 RSIMVQWIVKQCSDMGLQOETLFIGVGLLDRFLSKGSFKSERTLLIVGIASLILLATRIEE 446
Db  213 RGLIDWLVEVSEEYKLVSDTLITVNLIDRFMSH-NIEKRKLQLLGVTCMLIASKYEE 271

Qy  447 NOPYNSIRKRNFT-IQNLRYSRHEVVANEMLVQEVLNFKCFTPTFINFLWFYLKAARANP 505
Db  272 ---ISAPRLEEFCFITDNYYTRLEVLSMEIKVLNSLHPRLSVPPTKTFLRRFIRAAQASD 328

Qy  506 -----EVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLA 540
Db  329 KVPLIEMEYLANYFAELILTEYTFLRFLIPSLIAASAVFLA 368
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DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cell cycle; Cell division; Cyclin.
SQ   SEQUENCE 434 AA; 49345 MW; 018C758EBBD8D8BF CRC64;

Query Match            25.5%; Score 251; DB 10; Length 434;
Best Local Similarity  25.5%; Pred. No. 7.4e-09;
Matches  86; Conservative  67; Mismatches 142; Indels  42; Gaps  10;

Qy  250 SEKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGGSEFSE--KSSSDSPIS 307
            ::::::: ::  :::.::   :  :::  ::       :::::::::::     :::
Db   84 TRKYAAQIASSQKHSSEENK-----------------------PKIAAESFSVWEDDMEAANDKPVP 128

Qy  308 HSRSLYLQFKEQFCRSTIPNDFGSSCE-EEIHSEL---LRFDD------EEVEESYLR 355
            ::::::::::::::::::::::: :::  :::::     :::        :::::::
Db  129 MS----LEQTEKVSKGKDQMYIQEVEMEDIFEEAVIDIDGDDAKNHLAAVEVGDLFAN 184

Qy  356 LRERERSHAYMRDCAKAYCSRMDNTGLIPIRLRSIMVQWIVKQCCSDMGLQOEFLFLGVGLL 415
            :::::::::::::::::::::::::  :  :::::::::::::  :: ::::::::::::
Db  185 YRTME-----VNSCASPY-YMAQQADINERMRSILIDWLIEVHHKFELREETLFLTVNLI 238

Qy  416 DRFLSKGSFKSERTLLIVGIASLTLATRIEENQPYNSIRKRNFTIQNLRYSREVVAMEW 475
            ::: ::: ::::::::::::   :: :::::  : ::::::   :::::::::: :
Db  239 DRFLEKQGIVRKK-LQLVGLVAMLLACKYEE--VCAPLVEDLVLISDKAYTREVLEMES 295

Qy  476 LVQEVLNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAA 535
            ||||||||||||||  |||  ||  |||||||||||||| ||||||| ||| ||||||
Db  296 MMLNTLQFNMSVPTAVVFMRRYLKAAQCDRKLELLSPFMLVELCLVEYEMLKFPPSFIAAA 355

Qy  536 LVVLACIEHNKISAYQRVIKVHVHVRTTDNELPECVKSL 572
            ||| |||| |||  | |||||||||||||| |||
Db  356 AIYTAQTTLIGVQQWSKTCEVHTTYSEDQLLECSRSI 392
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RESULT 6
Q40337

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ID   Q40337        PRELIMINARY;       PRT;   428 AA.
AC   Q40337;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B-LIKE CYCLIN.
GN   CYCIIIMS.
OS   Medicago sativa (Alfalfa).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX   NCBI_TaxID=3879;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=ROOT NODULES;
RX   MEDLINE=95284356; PubMed=7766889;
RA   Savoure A., Feher A., Kalo P., Petrovics G., Csanadi G., Szecsi J.,
RA   Kiss K., Brown S., Kondorosi A., Kondorosi E.;
RT   "Isolation of a full-length mitotic cyclin cDNA clone CycIIIMs from
RT   Medicago sativa: Chromosomal mapping and expression.";
RL   Plant Mol. Biol. 27:1059-1070(1995).
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR   EMBL; X78504; CAA55272.1; -.
DR   HSSP; P30274; 1VIN.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR004367; Cyclin_C.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cell cycle; Cell division; Cyclin.
SQ   SEQUENCE 428 AA; 48809 MW; 2F6AAEBDF0C73413 CRC64;

Query Match            25.8%; Score 250; DB 10; Length 428;
Best Local Similarity  25.8%; Pred. No. 8.5e-09;
Matches  90; Conservative  68; Mismatches 121; Indels  70; Gaps  13;

Qy  250 SEKFSEEVSD--SLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGGSEFSEKSSSDSPIS 307
            :: :::  :   :  ::  :::::  :     ::  :   ::::::::::  ::::::::
Db   75 TRRFAAKIANTKTINAEGTTKRSNL-AKSSSNGFGDF---IFVDD----EIHKPVEDQPVP 126

Qy  308 HSRSLYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRFDDEEVEE------------S 352
            :        :::         :  ::::: :::: ::::::  :            :
Db  127 MA------LEQ----------TEPMISESDRMEEVEMEDIMEEPVMDIDTPDAND 165

Qy  353 YLRLRERERSHAYMRDCAKAYCSRMDNTGLI----------PRLRSIMVQWIVKQCSD 400
            :   :  ::  ::  :::::: :::  ::::          ::::::::::::: :::
Db  166 PLAVAE------YIED-LYSYYRKYESTSCVSPNYMAQQFDINERMRAILVDWLIEVHDK 218

Qy  401 MGLQOEFLFLGVGLLDRFLSKGSFKSERTLLIVGIASLTLATRIEE-NQPYNSIRKRNFT 459
            :  :: ::::::::::::: ::  ::::::::::::   :: :::::  : ::::::
Db  219 FDLMHETLFLTVNLIDRFLEKQSVVRKK-LQLVGLVAMLLACKYEEVSVP----PRLRSIMVQWIVKQCSD  274

Qy  460 IQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTSL 519
            :::::::::: :   :: ::::::::::::::  ||| || |||||||||||||| |||
Db  275 ISDRAYTRKEVLEMEKVMVNALKFNISVPTAYVFMRRFLKAAQADRKLELLAFFLIELSL 334

Qy  520 SDQTQLCFWPSTVAAALVVLACIEHNKISAYQRVIKVHVHVRTTDNELPEC 568
            ||| ||| ||||||  ||| |||| |||  | |||||||||||||| |||
Db  335 VEYAMLKFSPSQLAAAAVYTAQCTMYGVKQWSKTCEVHTTNYSEDQLLEC 383
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RESULT 7
Q9ZU09

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ID   Q9ZU09        PRELIMINARY;       PRT;   444 AA.
AC   Q9ZU09;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CYCLIN 3A.
GN   F18G18.15.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Huang E.N., Dedhia N., de la Bastide M., Habermann K., Matero A.,
RA   Preston R., Shekher M., Rodriguez M., Nascimento L., Spiegel L.A.,
RA   Schutz K., Shah R., Swaby I., Vil M.D., O'Shaughnessy A.,
RA   Parnell L.D., McCombie W.R.,
RT   "Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR   EMBL; AC006258; AAC98445.1; -.
DR   HSSP; P30274; 1VIN.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR004367; Cyclin_C.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cell cycle; Cell division; Cyclin.
SQ   SEQUENCE 444 AA; 50435 MW; 9335743BE4E52278 CRC64;

Query Match            24.8%; Score 249.5; DB 10; Length 444;
Best Local Similarity  24.8%; Pred. No. 9.7e-09;
Matches 114; Conservative  75; Mismatches 150; Indels 121; Gaps  19;

Qy   99 KETIGDSKER-----RITRSYSKLIHKEKEGDEIEVSESSCVDSNSGAGLRRLNVKGNKIND 154
            ::  : :::     ::::: :::  ::     :: ::  :         :: ::
Db   13 KEAISTSKIRDNNVAVTRSRAK-----------ALGVSNSPSPSKPAFKIE-TKRVARPSNKRMA 63

Qy  155 NDEISFSRSDVTFAGHVSNSRS---LNFESENKESDVVSIGVEYCSKFGSVIGGADNE 211
            :::  :
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Db     64 SDNIT------------VCNQKRRAVLKDVTNTLAESIISTEGCNVKVACK----RGGKETK 108
            :||  :  |: |  |  :||:|:|:: |  | |:|:   |  :|: | |
Qy    212 EIEISKPSSFVEADSSIGSAKELKPELEIVGCVSDLACSEKFSEEVSDSLDDESSEQRSE 271

Qy    109 QIE---EDGLVDVD---GEKSKLAEDLSKIRMV------------------ESLDASAKQKLV 148
            |||    |:|:|:|    |::||  |:|::            :|| : : |:
Db    272 IYSQYSPDFDYSDYTPSIFFDSGSEFSEKSSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGS 331

Db    149 DCAEEDRSDVTDCVQIVDIDSGVQ----------------DPQFC----SLYAA 182
            |   |||  | |  |  |||                     || |     ||  |
Qy    332 SCEEEIH-SELLRFDDEEVEESYLRLRERERSHAYM------RDCAKAYCSRMDNTGLIPRL 386

Qy    183 SIYDSINVAEL----------------EQRPSTSYMVQVQRD----------IDPTM 213
            :| :|   | |                 ||| | || : :            |||
Db    387 RSIMVQWIVKQCSDMGLLQQEFLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEE 446

Db    214 RGTLIDWLVEVSEEYKLVSDTLYLTIVNLIDRFMSHNYIEKQK-LQLLGITCMLIASKYEE 272
            : | :|:||:||||| || :|| : :| ||||  ||  ||:| |  |: | ||:|||:|||
Qy    447 NQPYNSIRKRNFT-IQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANP 505

Db    273 ---ISAPRLEEFCFITDNTYTRLEVLSMEIKVLNSLIHPRLSVPTTKTFLRRFIRAAQASD 329
            :: : :|  |: ||::| | |::  :|    |:|:|    :||:  | | | ||::||  |:
Qy    506 ------EVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVIA 540

Db    330 KVPLIEMEYLANYFAELTLTEYTFLRFLPSLIAASAVFLA 369


RESULT 8

ID     O15996          PRELIMINARY;     PRT;      458 AA.
AC     O15996;
DT     01-JAN-1998 (TrEMBLrel. 05, Created)
DT     01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE     CYCLIN A.
GN     HPCYCA.
OS     Hemicentrotus pulcherrimus (Sea urchin).
OC     Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC     Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC     Hemicentrotus.
OX     NCBI_TaxID=7650;
RN     [1]
RP     SEQUENCE FROM N.A.
RA     Kurokawa D., Akasaka K., Mitsunaga-Nakatsubo K., Shimada H.;
RT     "Cloning of Cyclin A cDNA of sea urchin, Hemicentrotus pulcherrimus.";
RL     Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
CC     -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR     EMBL; AB008364; BAA22991.1; -.
DR     HSSP; P30274; 1VIN.
DR     InterPro; IPR004366; Cyclin.
DR     InterPro; IPR004367; Cyclin_C.
DR     InterPro; IPR003015; HLH_Myc.
DR     Pfam; PF00134; cyclin; 1.
DR     Pfam; PF02984; cyclin_C; 1.
DR     SMART; SM00385; CYCLIN; 2.
DR     PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW     Cell cycle; Cell division; Cyclin.
SQ     SEQUENCE 458 AA; 51308 MW; DFFF9A14A2C68A63 CRC64;

Query Match             8.3%;  Score 246;  DB 5;   Length 458;
Best Local Similarity  27.7%;
Matches   114;  Conservative   61;  Mismatches 156;  Indels  80;  Gaps  17;

Qy    179 FESENKESDVVSVTSGVEYCSKPGSVTGGADNE-EIEISKPSSFVEADSSIGSAKELKPE 237
            |: :|:|||:|||| || :|:|| :::|| |:   |:|:||| ::|| : |:|:| | |
Db     78 FQDENAH----------------SRIPGDKPFGIPSAGAAPAFSIHVDTTSSVQSSTS---- 120

Qy    238 LEIVGCVSDLACSEKFSEEVSDSLDDESS-----EQRSEIYSQYSDF-DYSDYTPSIFFD 291
            : | | :| |  |::  :: :||| ||       ||| || | :||  |:||:||| |
Db    121 ------TSIKSTDKENEHI---LLDNALSLPVPQAQRIPLRT---FPDVEDNNVSL--- 164

Qy    292 SGSEFSEKSSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRFDDEEVEE 351
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Db    165 -----NEESLYSSEFSPMLLDTSL----DAKCISPRTVDI--------RDLSLGEPEYAEE 208
            :|| :|  ||:: |||:|  |      ||| |||  |:         |: | | ||: ||
Qy    352 SYLRLRERER----SHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLLQQET 407

Db    209 IYQYLKTAESKHRPKHGYMR----KQPDIYN--SMRCIIVDWLVEVSEEYRLHNET 258
            :: | :::|| | | || ||     : |  :   :: | |:|:||:|||| |||||
Qy    408 LFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEENQPYNSIRKRNFTIQNLRYSR 467

Db    259 LYLAAAFIDRFLSQMSVLRAK-LQLVGTASMFVASKYEEIIYPPDV--KEFVVITDDTYSI 315
            | :   | ||||| :|:||:| |||:| :|:::|||||| |:||||   || |||||:|:
Qy    468 HEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTSLSDQTQLCF 527

Db    316 KQVLRMEHIILKVLSFDLAAPTINSFLPRFIKAAQANSKTEHLTQYLAELTLQEYDFIKY 375
            |:| | |:|||| | |||||| ||||| ||||||||| ||||||||||||||| | ||||
Qy    528 WPSTVAAALVVLACIEHNKISAYQRVIKVHVRITDNELPE---CVKSLDWL 575

Db    376 APSMIAASAVCLA----NHTLNNEEWTPTMAHYTDYQLGDIYPCVQDLHQL 422


RESULT 9

ID     Q39068          PRELIMINARY;     PRT;      429 AA.
AC     Q39068;
DT     01-NOV-1996 (TrEMBLrel. 01, Created)
DT     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE     CYCLIN 2A PROTEIN.
GN     CYC2A.
OS     Arabidopsis thaliana (Mouse-ear cress).
OC     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC     eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX     NCBI_TaxID=3702;
RN     [1]
RP     SEQUENCE FROM N.A.
RC     STRAIN=COLUMBIA; TISSUE=CELL SUSPENSION;
RX     MEDLINE=95062258; PubMed=7972055;
RA     Ferreira P.C.G., Hemerly A.S., De Almeida Engler J., Bergounioux C.,
RA     Burssens S., Van Montagu M., Engler G., Inze D.;
RT     "Three discrete classes of Arabidopsis cyclins are expressed during
RT     different intervals of the cell cycle.";
RL     Proc. Natl. Acad. Sci. U.S.A. 91:11313-11317(1994).
RN     [2]
RP     SEQUENCE FROM N.A.
RC     STRAIN=COLUMBIA; TISSUE-CELL SUSPENSION;
RA     Van Montagu M.;
RL     Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
CC     -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR     EMBL; Z31400; CAAB3275.1; -.
DR     HSSP; P30274; 1VIN.
DR     InterPro; IPR004366; Cyclin.
DR     InterPro; IPR004367; Cyclin_C.
DR     Pfam; PF00134; cyclin; 1.
DR     Pfam; PF02984; cyclin_C; 1.
DR     SMART; SM00385; CYCLIN; 2.
DR     PROSITE; PS00292; CYCLINS; 1.
KW     Cell cycle; Cell division; Cyclin.
SQ     SEQUENCE 429 AA; 49232 MW; B88EB527E40ADBEC CRC64;

Query Match             8.2%;  Score 243.5;  DB 10;  Length 429;
Best Local Similarity  24.9%;
Matches    91;  Conservative   70;  Mismatches 155;  Indels  49;  Gaps   9;

Qy    222 VEADSSIGSAKELKPELEIVGCVSDLACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDY 281
            |  ::|| |:|::       |  |: |:|| | :|: ::| |::  | ||:||:||:|||
Db     57 VNKKGSLLSNKQEEEE--------GCQKKKFDSLRPSVTRSGVEEETNKKLKPSVPSA 106

Qy    282 SDYTPSIFFDSGSEFSEKSSSSDSPISHS-RSLYLQFKEQFCRSTIPNDFGSSCEEEIHSE 340
            :|:  :| ||| |   |  :|  |||:|  |||: :: |: |||:||:| |:: |||||:|
Db    107 NDFGDCIFID----EEEATLDLPMPMSLEKPYIE--------------ADPMEEVEME 146
```

Qy 341 LLRFDDEEVEESYLRLRERERSHAYMRDCAKAYCSRMDNTGLIP--------RLRS 388
Db 147 DVTVEEPIVDIDVLDSKNSLAAVEYVQD-LYAFYRTMERFSCVPVDYMMQQIDLNEKMRA 205

Qy 389 IMWQWIVKQCSDMGLQQETFLGVGLLDRFLSKGSFKSERTLILVGIASLITLATRIEE-N 447
Db 206 ILIDWLIEVHDKFDLMNETLFLTVNLIDRFLSKQNVMRKK-LQLVGLVALLLACKYEEVS 264

Qy 448 QPYNSIRKRNFTIQNLRYSRHHVVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEV 507
Db 265 VP---VVEDLVLISDKAYTRNDVLEMEKTMLSSTLQFNISLPTQYPFLKRFLKAAQADKKC 321

Qy 508 ERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHHKISAYQRVIKVHVRTDNELPE 567
Db 322 EVLASFIELALVEYEMLRFPPSLLAATSVYTAQCTLDGSRKWNSTCEFHCHYSEDQLME 381

Qy 568 CVKSL 572
Db 382 CSRKL 386

RESULT 10

ID   P90681   PRELIMINARY;   PRT;   445 AA.
AC   P90681;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CYCLIN A.
OS   Asterina pectinifera (Starfish).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC   Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
OX   NCBI_TaxID=7594;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tachibana K., Uchida T., Kishimoto T.;
RT   "Differential regulation of cyclin A/cdc2 and cyclin B/cdc2 during
RT   meiotic and early cleavage cycles in starfish eggs.";
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR   EMBL; D89723; BAA14010.1; -.
DR   HSSP; P20248; 1JSU.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR003015; HLH_Myc.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
DR   PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW   Cell cycle; Cell division; Cyclin.
SQ   SEQUENCE 445 AA; 49451 MW; 74D8749FDC954A31 CRC64;

Query Match   8.2%; Score 243; DB 5; Length 445;
Best Local Similarity   23.9%;
Matches 111; Conservative 72; Mismatches 169; Indels 112; Gaps 16;

Qy 159 SFSRSDVTFAGHVSNSRSLNFESENKESDVVSVISGVEYC 198
Db   4 AFSENPLTV--DVENSQNAPGQTRKTKREDAGRGNGPQOACKRAALGTLSTNVTRKQPSRA 61

Qy 202 GSVTGGAD-----NEIEISRPSSFVEADSSLGSAAKELKPELEIVGCVSDLACSEKFSEE 256
Db 62 AKQSGFADGFYNYQDENAFARRA---AGKSTGSCGFALP-----PTASQPSFSIH 108

Qy 257 VSDSLDDESSEQRSEIYSQYSDFDYTPSIFFDSGSEFSEKSSSDSP-----ISHS 309
Db 109 I-DPVEPAPSRARF---------------DEEVEESYLRLRER 142

Qy 310 RSLYLQFKEQFCRSTIPNDFGGSCEEEIHSELLRFD-----------LKEQKPTELPLDPIGYFVTRS 359
Db 143 RKTALRTVFTLDESASPMVLDTSLSEENTAQATIEDIDNSDGVFGVPEYAEDIYEYLREA 202

RESULT 11

ID   O24073   PRELIMINARY;   PRT;   452 AA.
AC   O24073;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CYCLIN.
GN   CYCMS3.
OS   Medicago sativa (Alfalfa).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX   NCBI_TaxID=3879;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95375541; PubMed=7647566;
RA   Meskiene I., Boegre L., Dahl M., Pirck M., Ha D.T.C., Swoboda I.,
RA   Heberle-Bors E., Ammerer G., Hirt H.;
RT   "cycMs3, a novel B-type Alfalfa cyclin gene is induced in the G0-to-G1
RT   transition of the cell cycle.";
RL   Plant Cell 7:759-771(1995).
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR   EMBL; X85783; CAA59768.1; -.
DR   HSSP; P30274; 1VIN.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR004367; Cyclin_C.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
KW   Cell cycle; Cell division; Cyclin.
SQ   SEQUENCE 452 AA; 51134 MW; D4111B0C85706C1 CRC64;

Query Match   8.2%; Score 242.5; DB 10; Length 452;
Best Local Similarity   27.0%;
Matches 110; Conservative 68; Mismatches 148; Indels 81; Gaps 15;

Qy 360 ERSH-----AYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETFLFLGVGLL 415
Db 203 ELRNRPKPGYMR---------KQPDITSGMRSILVDWLIEVGEEYRLHNETLYLAVSYI 252

Qy 416 DRFLSKGSFKSERTLILVGIASLITLATRIEENQP-----YNSIRKRNFTIQNLRYSRHEV 470
Db 253 DRFLSQMSVLRSK-LQLVGAASMFLAAKFEEIYPPEVNEFVVITDDTYTVK-----QV 304

Qy 471 VAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPS 530
Db 305 LRMEHLILKVLSFDVAVPTANAFLSRYLKAAKADSRNGTSSQYLAELTLPDCEYIKYIPS 364

Qy 531 TVAAALVVLACIEHHKIS--AYQRVIKVHVRTDNELPECVKSL 572
Db 365 TIAAAAV---CLANYLSGTAWTPMLEKHSGYNLEDIAPCVRDL 405

Qy 163 SDVTFAGH----------VSNSRSLNFESENKESDVVSVISGVEYCSKFGSVTGGADNEEIE 214
Db 24 SDVTLPHKKRAILQQVTNCGVNTER-----SCLNPTEIQAK------KRK 64

Qy 215 ISKPSSFVEADSSLGSAAKELKPELEIVGCVSDLACSEKFSEEVS--DSLDDESSEQRSEI 272
Db 65 VAKPAQ-PHVSNEVPSAAELPPFIADSKPVSSMEMRLRSSEDPRCLDDLEDNAPFRMSS- 122

Qy 273 YSQYSDFDYTPSIFFDSGSEFSEKSSSDSPISHSRSLVLQFKEQFCRSTIPNDFGSS 332
Db 123 -------------NQCGTNNLLQSQTSRIS-ARPLSSQKRASQIVAAKKGNISEL 164

Qy 333 CEEEIHSEL----LRFDDEEVEESY-----LRLRERERSHAYMRDCAKAYCSRMDNT- 380
Db 165 LDVSKHPDVADIDADPEDPQLCSHYAADIYDHLRYAELSR-------RPYPNFMETVQ 215

Qy 381 -GLIPLRLSIMVQWIVKQCSDMGLQQETFLGVGLILDRFLSKGSFKSERTLILVGIASLT 439

Db   216   QDITPSMRAILLVDWLIVEVSEGYKLQANTLSLTVLIDWFLSKNCIERER-LQLLIGTCML   274
           ::: :| : || | || || :|| : | | | | ||:| : | : | || : |||:|
Qy   440   LATRIEENQPYNSIRKRNFT-IQNLRYSRHEVVAMEWLVQEVLNFKCTPTTIENFLWFYL   498

Db   275   IATKYEE---INAPRIKDFCFIQDNTYTKEEVVKLESLVLKSSSYQLIFAPTTKTFLRRFL   331
           |||| || | || : | || : | | | | || | ||:
Qy   499   KAARA------NPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLA   540

Db   332   RAAQASYKRPSIELEYLANYLAELTLMNYGFLNFLPSMVAASSVFLA   378

RESULT 12

Q41731

ID   Q41731;   PRELIMINARY;   PRT;   424 AA.
AC   Q41731;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CYCLIN IIIZM.
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B73; TISSUE=EAR;
RX   MEDLINE=94316698; PubMed=8041798;
RA   Renaudin J., Colasanti J., Rime H., Yuan Z., Sundaresan V.;
RT   "Cloning of four cyclins from maize indicates that higher plants have
RT   three structurally distinct groups of mitotic cyclins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:7375-7379(1994).
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR   EMBL; U10076; AAA20236.1; -.
DR   HSSP; P30274; 1VIN.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR004367; Cyclin_C.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cell cycle; Cell division; Cyclin.
SQ   SEQUENCE   424 AA;   47777 MW;   C3AEF1DC5D36B7F5 CRC64;

Qy   178   NFESENKESDVVSISGVEYC------------SKFGSVTGGADNEEIEISKPS-SFVEAD   225
           || | | | | | : || | | ||::| || | ::|
Db   3   NLRSQNCHQGV--AMEGVKFAPEKANTNRRALSDIKNIIGG-PHQHLAVSKRALSEKPA   59

Qy   226   SSLGSAKELKPELEIVGCVSDLACSEKFSEEVSDS-----LDDESSEQRSEIYSQYSDFD   280
           ||| |||||||||||||||||||||||||||||| || ||||||||||||
Db   60   AAAANAKDQ-----AGFVGHRPVTVRKFAATLATQPTIVALLDPIGSERLKR------NAD   107

Qy   281   YSDYTPSIFFDSGSEFSEKSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSCEEIHSE   340
           |:|:|||||||||||||||:|||||||||:|||||||||||||||||||||||||||
Db   108   TAFHTPA--------DMESTKMTDDSPL-----PMVSEMDEMSPE   140

Qy   341   LLRFDDEEVEESYLRLRERERSHA------------YMRDCAKAYCSRMDNTGLIP-----   384
           |:|||||||||||:||| | | ||| |||| |||
Db   141   LKEIEMEDIEEAAPDIDSGDAGNSLAVADYDEIYRFY-RKIEGASCVPTNYMSSQTDIN   199

Qy   385   -RLRSIMVQWIVKQCSDMGLQOQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLITATR   443
           |:|| ||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db   200   EKMRGLIIDWLIEVHYKLELLEETLFLTVNIIDRFLARENVRKK-LQLAGVTAMLLACK   258

Qy   444   IEE-NQPYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPITFNFLWFYLKAAR   502
           | || :| ||| | || | | | | | | || | || |
Db   259   YEEVSVP---VVEDLLICDRAYTRADILEMERRIVNTLNFNMSVPTPYCFMRFLKAAQ   315

RESULT 13

Q9SHP1

ID   Q9SHP1   PRELIMINARY;   PRT;   429 AA.
AC   Q9SHP1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PUTATIVE CYCLIN 2.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.J., Moffat K.S.,
RA   Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA   Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA   Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA   Salzberg S.L., Fraser C.M., Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Lin X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR   EMBL; AC007509; AAD32049.1; -.
DR   HSSP; P30274; 1VIN.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR004367; Cyclin_C.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cell cycle; Cell division; Cyclin.
SQ   SEQUENCE   429 AA;   49242 MW;   B6E2DCFC4ED65770 CRC64;

Qy   503   ANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISAYQRVIKVHVRTD   562
           |||||||||||||||||||||||||||||||||||||||||| | : | : |
Db   316   SEKKLELLSFFMIELSLVEYEMLQFCPSMLAAAIYTAQCTINGFKSWNKCCELHTRYSE   375

Qy   563   NELPECVKSL   572
           : | | |
Db   376   EHLMVCSRMM   385

Query Match   Best Local Similarity   24.9%;
               Conservative   70%;   Matches   91;   Mismatches   155;   Indels   49;   Gaps   9;

Qy   222   VEADSSLGSAKELKPELEIVGCVSDLACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDY   281
           | | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   57   VNKRGSLLSNKQEEEE--------GCQKKKFPDSLRPSVTRSGVEETNKKLKPSVPSA   106

Qy   282   SDYTPSIFFDSGSEFSEKSSSDSPISHS-RSLYLQFKEQFCRSTIPNDFGSSCEEIHSE   340
           ||:|||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   107   NDFGDCIFID-----EEEATLDLPMEMSLEKPYIE------------ADPMEEVEME   146

Qy   341   LLRFDDEEVEESYLRLRERERSHAYMRDCAKAYCSRMDNTGLIP-------------RLRS   388
           ||||||||||||||||||||| | | ||| | |: | : |
Db   147   DVTVEEPIVDIDVLDSKNSLAAVEYVQD-LYAFYRTMERFSCVPVDYMMQQIDLNEKMRA   205

Qy   389   IMVQWIVKQCSDMGLQOQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLITATRIEE-N   447

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Db  206 ILIDWLIEVHDKFDLINETLFLTVNLIDRFLSKQNYMRKK-LQLVGLVALLACKYEEVS 264
         |::|  |::::
Qy  448 QPYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNELWFYLKAARANPEV 507
Db  265 VP---VVEDLVLISDKAYTRNDVLEMEKTMLSTLQFNISLPTTQYPFLKRFLKAAQADKKC 321
Qy  508 ERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISAYQRVIKVHVRTTDNELPE 567
Db  322 EVLASFLIELALVEYEMLRFPPSLLAANTSVYTAQCTLDGSRKWNSTCEFHCHYSEDQLME 381

Qy  568 CVKSL 572
         | : |
Db  382 CSRKL 386
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RESULT 14
ID   O62573   PRELIMINARY;   PRT;   462 AA.
AC   O62573;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CYCLIN A.
GN   CYCA.
OS   Sphaerechinus granularis (Purple sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
OC   Sphaerechinus.
OX   NCBI_TaxID=39374;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYO;
RA   Geneviere A.M., Marques F., Schatt P., Picard A.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR   EMBL; AJ224985; CAA12275.1; -.
DR   HSSP; P30274; 1VIN.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR004367; Cyclin_C.
DR   InterPro; IPR003015; HLH_Myc.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW   Cell cycle; Cell division; Cyclin.
SQ   SEQUENCE 462 AA; 51593 MW; EA5001B2E3D0788F CRC64;

Query Match   8.1%; Score 239.5; DB 5; Length 462;
Best Local Similarity   26.8%; Pred. No. 4.7e-08;
Matches 102; Conservative 53; Mismatches 142; Indels 83; Gaps 14;

```
Qy  179 FESENKESDDVVSVIGVEYCSKFGSVTGGADNE-EIEISKPSSFVEADSSLGSAKELKPE 237
         :|:| |
Db   79 FQDENAH------SRIPQGKPFGIPSAAAAPAFSIHVDPTSTYVQPOTASTSIKSTDKE 131
Qy  238 LEIVGCVSDLACS---------EKFSEEVSD---SLDDESSEQRSEIYSQYSDFDYS 282
Db  132 NEHI--LLDIALSLPVPPQAQRIPLRSSGPDVEDNNVSLNEES----------LTSS 176
Qy  283 DYTPSTFPDSGSEFSEKSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSCEEIHSELL 342
         :|:| :
Db  177 EYSPMLL---DTSLDAKCISPQTVVAERDLSLGEPEY-------------SEEIY---- 215
Qy  343 RFDDEEVEESYLRLRERER--SHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSD 400
Db  216 --------QYLKTAELKHREKHGYMR------KQPDITN--NMRCILIDWLVEVSEE 256
Qy  401 MGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEENQPYNSIRKRNFTI 460
Db  257 YRLHNETLYLAAAFIDRFLSQMSVLRAK-LQLVGTASMFVASKYEEIYPPDV--KEFYI 313
```

```
Qy  461 QNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTSLS 520
         :: |  | :|  || :| :::|  || ||| | ||||:::|| :| ||||:||:|:| :|
Db  314 TDDTYSIKQVLRMEHLILKVLSFDLAAPTINCFLPRFLKAAQANSKTEHLTQYLAELTLQ 373
Qy  521 DQTQLCFWPSTVAAALVVLA 540
         :  || |:|| | || | ||
Db  374 KYDFIKYVPSMIAASRVCLA 393
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RESULT 15
ID   Q9NIP5   PRELIMINARY;   PRT;   457 AA.
AC   Q9NIP5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CYCLIN A.
OS   Strongylocentrotus purpuratus (Purple sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC   Strongylocentrotus.
OX   NCBI_TaxID=7668;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yoon J.W., Winkler M.M.;
RT   "Multiple levels of regulation of cyclin A and B expression during
RT   early sea urchin development.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF205358; AAF67075.1; -.
DR   HSSP; P20248; 1JSU.
DR   InterPro; IPR004366; Cyclin.
DR   InterPro; IPR003015; HLH_Myc.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SQ   SEQUENCE 457 AA; 51250 MW; B53D5332A4033BC66 CRC64;

Query Match   8.1%; Score 239; DB 5; Length 457;
Best Local Similarity   32.8%; Pred. No. 5e-08;
Matches 78; Conservative 39; Mismatches 97; Indels 24; Gaps 7;

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Qy  345 DDEEVEESYLRLRERER----SHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSD 400
         : :| : |
Db  201 EPEYAEEIYQYLKTAESKHRRKHGYMR------KQPDITN--SMRCILVDWLVEVSEE 250
Qy  401 MGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEENQPYNSIRKRNFTI 460
         | ||||:|||:|| | ||
Db  251 YRLHNETLYLAAAFIDRFLSQMSVLRAK-LQLVGTRASMFVASKYEEIYPPDV--KEFYI 307
Qy  461 QNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTSLS 520
         :: |  | :|  ||
Db  308 TDDTYSIKQVLRMEHLILKVLSFDLAAPTINSFLPRFIKAAKANSKTEHLTQYLAELTLQ 367
Qy  521 DQTQLCFWPSTVAAALVVLACIEHNKISAYQRVIKVHVRTTDNELPE---CVKSLDWL 575
Db  368 EYDFIKYAPSMIAASAVCLA---NHTLNNEEWTPTMAHYTDYQLGDIYPCVQDLHQL 421
```

Search completed: July 23, 2002, 14:25:30
Job time: 249 sec

```
GenCore version 4.5
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OM protein - protein search, using sw model

Run on:            July 23, 2002, 14:22:26 ; Search time 13.46 Seconds
                   (without alignments)
                   1662.697 Million cell updates/sec

Title:             US-09-821-839-2
Perfect score:     2952
Sequence:          1 MKEIAMRNSKRKPEPTPFAG............RTTDNELPECVRSLDWLLGQ 578

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched:          105224 seqs, 38719950 residues

Total number of hits satisfying chosen parameters:  105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         SwissProt_40:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

```
                                                      SUMMARIES
Result          %
No.   Score  Match  Query Length  DB  ID          Description
----  -----  -----  ------------  --  --          -----------
  1   262.5    8.9      434        1  CG2B_MEDVA   medicago va
  2   252.5    8.6      328        1  CG2B_MEDSA   medicago sa
  3   244      8.3      328        1  CG1B_MEDVA   medicago va
  4   233.5    7.9      419        1  CG2B_ORYSA   oryza sativ
  5   227.5    7.7      341        1  CG2A_DAUCA   daucus caro
  6   223.5    7.6      473        1  CG21_ANTMA   antirrhinum
  7   222.5    7.5      257        1  CG22_SOYBN   glycine max
  8   220      7.5      426        1  CG2A_PATVU   patella vul
  9   217.5    7.4      392        1  CGB2_RANJA   rana japoni
 10   217.5    7.4      415        1  CG2A_XENLA   xenopus lae
 11   213      7.2      454        1  CG21_SOYBN   glycine max
 12   212.5    7.2      421        1  CGA1_MOUSE   mus musculu
 13   212      7.2      422        1  CG2A_SPISO   spisula sol
 14   211      7.1      421        1  CG2A_MESAU   mesocricetu
 15   210.5    7.1      406        1  CGA2_BOVIN   bos taurus
 16   209      7.1      418        1  CGA1_XENLA   xenopus lae
 17   207.5    7.0      432        1  CGA2_HUMAN   homo sapien
 18   206      7.0      430        1  CGA2_HUMAN   homo sapien
 19   202      6.8      441        1  CGB1_MOUSE   mus musculu
 20   202      6.8      420        1  CG2A_XENLA   xenopus lae
 21   201      6.8      420        1  CG2A_CHLVR   chlorohydra
 22   201      6.8      465        1  CGA1_HUMAN   homo sapien
 23   200      6.8      395        1  CG2B_CHICK   gallus gall
 24   200      6.8      409        1  CGB2_ARBPU   arbacia pun
 25   199.5    6.8      399        1  CG2B_CHICK   gallus gall
 26   199.5    6.8      422        1  CGA2_MOUSE   mus musculu
 27   197      6.7      482        1  CG23_SCHPO   schizosacch
 28   196      6.7      429        1  CGB1_MESAU   mesocricetu
 29   195      6.6      398        1  CGB2_HUMAN   homo sapien
 30   194.5    6.6      423        1  CGB1_RAT     rattus norv
 31   194.5    6.6      398        1  CGB2_MOUSE   mus musculu
 32   193.5    6.6      428        1  CG2B_ARATH   arabidopsis
 33   191.5    6.5      397        1  CGB1_XENLA   xenopus lae
 34   191.5    6.5      436        1  CG2B_DICDI   dictyostell
 35   191      6.5      434        1  CGB1_HUMAN   homo sapien
 36   191      6.5      460        1  CG24_YEAST   saccharomyc
 37   190      6.4      429        1  CGB1_CRILO   cricetulus
 38   189.5    6.4      428        1  CGB1_SPISO   spisula sol
 39   189      6.4      491        1  CG2B_DROME   drosophila
 40   187.5    6.4      403        1  CG2A_CHICK   gallus gall
 41   187      6.3      392        1  CGB2_XENLA   xenopus lae
 42   187      6.3      478        1  CGB3_CHICK   gallus gall
 43   184.5    6.2      391        1  CG21_EMENI   emericella
 44   184.5    6.2      404        1  CGA1_CARAU   carassius a
 45   183.5    6.2      404        1  CG21_CARAU   carassius a
      183.5    6.2      388        1  CGE2_HUMAN   homo sapien
      179.5    6.1      404        1  CG2B_MARGL   marthasteri
                                   1  CGE2_MOUSE   mus musculu
```

ALIGNMENTS

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RESULT       1
ID   CG2B_MEDVA
AC   P46278;
CG2B_MEDVA           STANDARD;      PRT;    434 AA.
ID   CG2B_MEDVA
AC   P46278;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   G2/mitotic-specific cyclin 2 (B-like cyclin) (CycMs2).
OS   Medicago varia.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX   NCBI_TaxID=36902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. A2;
RX   MEDLINE=95375541; PubMed=7647566;
RA   Meskiene I., Boegre L., Dahl M., Pirck M., Ha D.T.C., Swoboda I.,
RA   Heberle-Bors E., Ammerer G., Hirt H.;
RT   "cycMs3, a novel B-type alfalfa cyclin gene, is induced in the
RT   G0-to-G1 transition of the cell cycle.";
RL   Plant Cell 7:759-771(1995).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC       (MITOSIS) TRANSITION.
CC   -!- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC       SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC       MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC       SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC   -!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC       ABRUPTLY DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X82040; CAA57560.1; -.
DR   HSSP; P20248; 1FIN.
DR   InterPro; IPR000553; Cyclin.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis.
SQ   SEQUENCE   434 AA;  49367 MW;  644EF0A2681A4C32 CRC64;

Qy   292 SGSEFSEKSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSC---------------- 333

Query Match             8.9%;  Score 262.5; DB 1; Length 434;
Best Local Similarity  27.0%;  Pred. No. 6.9e-09;
Matches   86;  Conservative   57;  Mismatches 112;  Indels  63;  Gaps  8;
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RESULT 2

```
Qy    92  SQQSYAEKTKNSPLN------------------
              :.:||:.|::
Db   134  EHTEPMHSDPLEMEEVEMEDIEGEMILDIDSCDANNSLAVVEYIEDLHAYYRKIEYLGCV 193

Qy   334  --EEHSELLRFDEEVEE----------
            :.|||:.|||:|
Db         --SYLRLRERERSHAYMRDCAKAYC- 374

Db   375  --SRMD-NTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLI 431

Qy   194  SPTYMDDEQLDLNERMRAILVDWLIEVHDKFDLMQETLFLTVNLIDRFLAKQNVVRKK-LQ 252

Db   432  LVGIASLLTATRIEE-NQPYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFPTI 490

Db   253  LVGLVAMLLACKYEEVSVP---VVSDLIHIADRAYTRKDILEMEKLMLNTLQYNMSLPTA 309

Qy   491  FNFLWFYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISAY 550

Db   310  YVFMRRFLKAAQADKLELVAFFLVDLSLVEYEMLKFPPSLVAAAAVYTAQCTVSGEKHW 369

Qy   551  QRVIKVHVRTTDNELPEC 568

Db   370  NKTCEWHTNYSEDQLLEC 387
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ID   CG2B_MEDSA     STANDARD;      PRT;   328 AA.
AC   P30278;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   G2/mitotic-specific cyclin 2 (B-like cyclin) (CycMS2) (Fragment).
OS   Medicago sativa (Alfalfa).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX   NCBI_TaxID=3879;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93104677; PubMed=1307238;
RA   Hirt H., Mink M., Pfosser M., Boegre L., Gyoergyey J., Jonak C.,
RA   Gartner A., Dudits D., Heberle-Bors E.;
RT   "Alfalfa cyclins: differential expression during the cell cycle and
RT   in plant organs.";
RL   Plant Cell 4:1531-1538(1992).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC       (MITOSIS) TRANSITION.
CC   -!- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC       SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC       MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC       SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC   -!- TISSUE SPECIFICITY: ONLY EXPRESSED IN ORGANS WITH DIVIDING CELLS.
CC   -!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC       ABRUPTLY DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
```
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DR   EMBL; X68741; CAA48675.1; -.
DR   PIR; S29925; S29925.
DR   PIR; P00490; P00490.
DR   HSSP; P20248; 1JSU.
DR   InterPro; IPR000553; Cyclin.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
```

```
KW   Cyclin; Cell cycle; Cell division; Mitosis.
FT   NON_TER       1      1
SQ   SEQUENCE   328 AA;  37710 MW;  7E4CCB166B5D94E CRC64;
```

Query Match   78%;   Score 252.5;   DB 1;   Length 328;
Best Local Similarity   30.6%;   Pred. No. 1.9e-08;
Matches   78;   Conservative   48;   Mismatches   104;   Indels   25;   Gaps   6;

RESULT 3

```
Qy   335  EEIHSELLRFDDEEVEE-----------------------------------SYLRLRERERSHAYMRDCAKAYC---S 375

Db    31  EPMHSDPLEMEEVEMEDIEGEMILDIDSCDANNSLAVVEYIEDLHAYYRKIEYLGCVSPI 90

Qy   376  RMD-NTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLLLVG 434

Db    91  YMDEQLDLNERMRAILVDWLIEVHDKFDLMQETLFLTVNLIDRFLAKQNVVRKK-LQLVG 149

Qy   435  IASLLTATRIEE-NQPYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFPTIFNF 493

Db   150  LVAMLLACKYEEVSVP---VVSDLIHIADRAYTRKDILEMEKLMLNTLQYNMSLPTAYVF 206

Qy   494  LWFYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISAYQRV 553

Db   207  MRRFLKAAQADKLELVAFFLVDLSLVEYEMLKFPPSLVAAAAVYTAQCTVSGKIHWNKT 266

Qy   554  IKVHVRTTDNELPEC 568

Db   267  CEWHTNYSEDQLLEC 281
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ID   CG1B_MEDVA     STANDARD;      PRT;   428 AA.
AC   P46277;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   G2/mitotic-specific cyclin 1 (B-like cyclin) (CycMs1).
OS   Medicago varia.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX   NCBI_TaxID=36902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV A2;
RX   MEDLINE=95375541; PubMed=7647566;
RA   Meskiene I., Boegre L., Dahl M., Pirck M., Ha D.T.C., Swoboda I.,
RA   Heberle-Bors E., Ammerer G., Hirt H.;
RT   "cycMs3, a novel B-type alfalfa cyclin gene, is induced in the
RT   G0-to-G1 transition of the cell cycle.";
RL   Plant Cell 7:759-771(1995).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC       (MITOSIS) TRANSITION.
CC   -!- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC       SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC       MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC       SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC   -!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC       ABRUPTLY DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
```
```
DR   EMBL; X82039; CAA57559.1; -.
DR   HSSP; P20248; 1JSU.
DR   InterPro; IPR000553; Cyclin.
```

```
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis.
SQ   SEQUENCE   428 AA;  48754 MW;  D05A3296B85A0EA0 CRC64;

Query Match             8.3%;  Score 244; DB 1;  Length 428;
Best Local Similarity   25.4%;  Pred. No. 8.7e-08;
Matches   86;  Conservative  65;  Mismatches 139;  Indels   48;  Gaps  11;

Qy     250  SEKFSEEVSD--SLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGSEFSEKSSSSDSPI-  306
            :|:  ||||      ||| |  | |::|::|:|||:||: |||:|||| ||:|:|  |:
Db      75  TRRFAAKIASTKTSNAEGTTKRSNL-AKSSSNGFGDF---IFVDD---EHKPVEDQPVP   126

Qy     307  -------SHSRSLYLQFKEQPCRSTIPNDFGSSCEEEIHSELLRFDDEEVEESYLRLRE  358
                   | ||  ||| |  :|  ||:|||||:|||||||:| ||    ||||::||::
Db     127  MALEQTPMHSESDQMEEVEM------------EDIMEEPVMDITPDANDPLAVAEY   172

Qy     359  RERSHAYMRDCAKAYC----------SRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLG  411
            | |||  | |||  :              ||||:|::|:||::|:|:|  | ::|||::| :
Db     173  IEDLYSYYRKVESTSCVSPNYMAQQFD---INERMRAILVDWLIEVHDKFDLMHETLFLT   229

Qy     412  VGLLDRFLSKGFKSERTLLILVGIASLLTLATRIEE-NQPYNSIRKRNFTIQNLRYSRHEV  470
            ||||||||||| ||:|||:|:|  | |:|| |:|:| ||| ||::||||:||||:|::|||
Db     230  VNLIDRFLEKQSVVRRK-LQLVGLVAMLLACKYEEVSVP---VVGDLILISDRAYTRKEV  285

Qy     471  VAMEWLVQEVLNFKCFTPTIENFLWFYLKAARANPEVERKAKSLAVTSLSDQTOLCFWPS  530
            :|:|| ||||:||:|  |:|:|||| |||||:|    : ::| ||||||||| |||||:
Db     286  LEMEKVWNALKENISVPTAYVFMRRFLKAAQADRKLELLAFFLIELSLVEYAMLKFSPS  345

Qy     531  TVAAALVULACIEHNKISAYQRVIKVHVRTTDNELPEC  568
            ||   |:|:| |||||:::| ||:||||:||||||| |
Db     346  QLAAAAVYTAQCTMYGVKQWSKTCEWHTNYSEDQLLEC   383
```

```
CC   -!- ABRUPTLY DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC   -----------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
SQ   SEQUENCE   419 AA;  47572 MW;  A8774B56BD839A5B CRC64;

Query Match             7.9%;  Score 233.5; DB 1;  Length 419;
Best Local Similarity   24.9%;  Pred. No. 3.6e-07;
Matches   66;  Conservative  65;  Mismatches 113;  Indels   21;  Gaps   5;

Qy     325  IPNDFGSSCEEEIHSELLRFDDEEVEE--------------SYLRLRERSHAYMRDCAKA  372
            |||||||||:|||||| |:  | ||:||              :|  ||||  | |||||
Db     117  LPLPMMSEMDEVMGSELKEIEMEDIEEAAPDISCDANNSLAVVEVYDEIYSFYRRSEGL  176

Qy     373  YC----SRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGFSRKSER  428
                    ||||:|::|:||::|:|:|  | ::|||::| : ||||||||||| ||:|
Db     177  SCVSPNYMLSQNDINEKMRGILIDWLIEVHYKLELLDETLFLTVNIIDRFLARENVRKK   236

Qy     429  TLILVGIASLLTLATRIEE-NQPYNSIRKRNFTIQNLRYSRHEVVAAMEWLVQEVLNFKCFT  487
            |::|:|  | |:|| |:|: ||| ||::||||:||||:|::|||:|  ::||:||| |
Db     237  -LQLVGVTAMLLACKYEEVSVP---VVEDLILICDRAYTRTDILEMERMIVNTLQFDMSV   292

Qy     488  PTIPNFLWFYLKAARANPEVERKAKSLAVTSLSDQTOLCFWPSTVAAALVULACIEHNKI  547
            ||:|:|||||||||:|    : ::| ||||||||| |||||:||   |:|:| |||||:
Db     293  PTPYCFMRRFLKAAQSDKKLELMSFFIIELSLVEYEMLKFQPSMLAAAAIYTAQCTINGF  352

Qy     548  SAYQRVIKVHVRTTDNELPECVKSL  572
             || ||:||||:|||||||| |  |
Db     353  KSWNKCCELHTKYSEEQLMECSKMM  377
```

```
RESULT  4
ID   CG2B_ORYSA    STANDARD;    PRT;    419 AA.
AC   Q40671;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   G2/mitotic-specific cyclin 2 (B-like cyclin) (CycoS2).
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. PIN GAEW 53;
RA   Sauter M.;
RT   "Isolation and characterization of a cDNA encoding a mitotic cyclin of
RT   the CycB2 type from rice.";
RL   (In) Plant Gene Register PGR97-001.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. PIN GAEW 53;
RA   Sauter M., Mekhedov S.L., Kende H.;
RX   MEDLINE=95261415; PubMed=7742859;
RA   Sauter M., Mekhedov S.L., Kende H.;
RT   "Gibberellin promotes histone H1 kinase activity and the expression
RT   of cdc2 and cyclin genes during the induction of rapid growth in
RT   deepwater rice internodes.";
RL   Plant J. 7:623-632(1995).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC       (MITOSIS) TRANSITION.
CC   -!- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC       SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC       MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC       SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC   -!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
```

```
RESULT  5
ID   CG2A_DAUCA    STANDARD;    PRT;    341 AA.
AC   P25010;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   G2/mitotic-specific cyclin C13-1 (A-like cyclin) (Fragment).
OS   Daucus carota (Carrot).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX   NCBI_TaxID=4039;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. KURODAGOSUN;
RX   MEDLINE=91330894; PubMed=1831125;
RA   Hata S., Kouchi H., Suzuka I., Ishii T.;
RT   "Isolation and characterization of cDNA clones for plant cyclins.";
RL   EMBO J. 10:2681-2688(1991).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC       (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 AND CDK2 PROTEIN
CC       KINASES TO FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
CC       AND ARE ABRUPTLY DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC   -----------------------------------------------------------------
```

Left column — RESULT 6

```
DR   EMBL; X62819; CAA44631.1; -.
DR   PIR; S16521; S16521.
DR   HSSP; P20248; 1JSU.
DR   InterPro; IPR000553; Cyclin.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis.
FT   NON_TER       1      1
SQ   SEQUENCE   341 AA;  38724 MW;  5708DF4269C06F3F CRC64;
```

Query Match

Best Local Similarity   27.7%;   Score 227.5;   Pred. No. 6.3e-07;   DB 1;   Length 341;

Matches 89;   Conservative 51;   Mismatches 106;   Indels 75;   Gaps 14;

```
Qy  298 EKSSSDSPISHSRSLYL-QFKEQFC-------------RSTIPNDFGSSCEEIHSELLRFDD 346
Db   19 EISNNSSAVSGNEDLLCREFEVPKCVAQKKRKRGVKEDVGVDFGE---------------KFDD 67

Qy  347 EEVEES-------------YLRLRERERSHA------YMRDCAKAYCSRMDNTGLIPRLRSIMVQWIV 395
Db   68 PQMCSAVSVDSVYEYLKQMEMETKRRPMMNYIEQVQKDVTSNM--------RGVLVDWLV 118

Qy  396 KQCSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIASILTAIRIEENQPYNSIRK 455
Db  119 EVSLEYKLLPETLYLAISYVDRYLSVNVLNRQK-LQILGVSSFLIASKYEEIKPKN--V 174

Qy  456 RNFT-IQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEV------ER 509
Db  175 ADFVDITDNIYSQOEVVKMEADLLKTLKFEMGSPTVKTFLGF-IRAVQENPDVPKLKFEF 233

Qy  510 KAKSLAVTSLSDQTOLCFWPSTVAAALVVLA-------CIEHNKISAYQRVIKVHV 558
Db  234 LANYLAELSLLDYGCLEFVPSILAASVTFLARFTIRPNVNPWSIALQKCSGYK------- 286

Qy  559 RTTTDNELPECVKSL-DWLLGQ 578
Db  287 ---SKDLKECVLLHDLQMGR 304
```

```
RESULT   6
ID   CG21_ANTMA     STANDARD;      PRT;   473 AA.
AC   P34800;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   G2/mitotic-specific cyclin 1.
OS   Antirrhinum majus (Garden snapdragon).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
OX   NCBI_TaxID=4151;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94148008; PubMed=8313906;
RA   Fobert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.;
RT   "Patterns of cell division revealed by transcriptional regulation of
RT   genes during the cell cycle in plants.";
RL   EMBO J. 13:616-624(1994).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC       (MITOSIS) TRANSITION. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
CC       AND ARE ABRUPTLY DESTROYED AT MITOSIS.
```

Right column — RESULT 7

```
CC   -!- SUBUNIT: INTERACTS WITH THE CDC2 AND CDK2 PROTEIN KINASES TO FORM
CC       A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC       IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC   -!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC       ABRUPTLY DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC   ------------------------------------------------------------------------
```

```
DR   EMBL; X76122; CAA53728.1; -.
DR   PIR; S41709; S41709.
DR   HSSP; P30274; 1VIN.
DR   InterPro; IPR000553; Cyclin.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis.
SQ   SEQUENCE   473 AA;  52704 MW;  502CF173558763BA CRC64;
```

Query Match

Best Local Similarity   20.9%;   Score 223.5;   Pred. No. 1.7e-06;   DB 1;   Length 473;

Matches 98;   Conservative 99;   Mismatches 182;   Indels 89;   Gaps 18;

```
Qy  128 VSESSCVDSNSGAGLRRRLNYAKGNKIKDNDEISFSRSDVTFAGHVSNSRSLNFESENKESD 187
Db    7 VQQONRAEAAVPGAMKQKNIRAGEKKN-------RRALGDIGNLVTVRGV----DGRAKA 54

Qy  188 VVSVISGV--EYCSKF--GSVTGGADNEEIEISKPSSFVEA---DSSLGSAK------ 232
Db   55 IPQVSRPVTRSFCAQLLANAQTAAADNNKIN-AKGAIVVDGVLPDRVAAARVPAQKKAA 113

Qy  233 ELKPELEIVGCVSDLACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDS 292
Db  114 VVKPRPEEIIVISPDSVAERKEKPIEKEKAAEKSAKKK------------------APTL--- 155

Qy  293 GSEFSEKSSSDSPISHSRSLVLQFKEQFCRSTIPNDFGSSCEEIHSELLRFD-DEEVEE 351
Db  156 TSTLTAARSKAASGVK------TKTKEQIV------DIDAA--DVNNDLAVVEYVEDMYK 200

Qy  352 SYLRLRERERSHAYMRDCAKAYCSRMDNTGLIP-----RLRSIMVQWIVKQCSDMGLQQET 407
Db  201 FYKSVENESRPHDYM---------------GSOPEINEKMRAILIDWLVQVHHKFELSPET 246

Qy  408 LFLGVGLLDRFLSKGSFKSERTLILVGIASILTAIRIEE---NQPYNSIRKRNFTIQNLR 464
Db  247 LYLTINIVDRYLASET-TIRRELQLVGIGAMLIASKYEEIWAPEVHELV----CISDNT 300

Qy  465 YSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVERAKAKSLAVTSLSDQTO 524
Db  301 YSDKQILVMEKKILGALEWLITVPPYVFLVRFIKASMTDSDVENMVYFLAELGMMNYAT 360

Qy  525 LCFWPSTVAAALVVLACIEHNKISAYQRVIKVHVRFTDNELPECVKSL 572
Db  361 LIYCPSMIAAASVYAARCTLNKAPFWNETLQLHTGFSEPQLMDCAKLL 408
```

```
RESULT   7
ID   CG22_SOYBN     STANDARD;      PRT;   257 AA.
AC   P25012;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   G2/mitotic-specific cyclin S13-7 (B-like cyclin) (Fragment).
OS   Glycine max (Soybean).
```

```
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. AKISENGOKU; TISSUE=Root;
RX   MEDLINE=91330894; PubMed=1831125;
RA   Hata S., Kouchi H., Suzuka I., Ishii T.;
RT   "Isolation and characterization of cDNA clones for plant cyclins.";
RL   EMBO J. 10:2681-2688(1991).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC       (MITOSIS) TRANSITION.
CC   -!- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC       SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC       MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC       SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC   -!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC       ABRUPTLY DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN A/B SUBFAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X62303; CAA44188.1; -.
DR   HSSP; P30274; 1VIN.
DR   InterPro; IPR000553; Cyclin.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis.
FT   NON_TER       1      1
SQ   SEQUENCE   257 AA;  29376 MW;  C6D057F3C10ACEA5 CRC64;

RESULT 8
ID   CG2A_PATVU     STANDARD;      PRT;   426 AA.
AC   P24861;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   G2/mitotic-specific cyclin P.
OS   Patella vulgata (Common limpet).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
OC   Patelloidea; Patellidae; Patella.

Query Match             7.58;  Score 222.5;  DB 1;  Length 257;
Best Local Similarity   29.5%;  Pred. No. 8.6e-07;
Matches   56;  Conservative   43;  Mismatches   84;  Indels   7;  Gaps   3;

Qy   385  RLRSIMYQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLITATRI  444
               ::|:|:|  | |||:||  :  | |||:| ::|    | |||:||::| :::|:| :|:|
Db    28  RMRAILVDWLIDVHTKFELSLETLYLTINIIDRFLAVKTV--PRRELQVGISAMLMASKY   86

Qy   445  EENQP--YNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTPIFNFLWFYLKAAR  502
             ||||    :|:| | ::|| |::  ||| :|| :::| | :::|| | | | ||||   ||
Db    87  EEIWPPEVNDF----VCLSDRAYTHEQILAMEKTILNKLEWLTVPFPFVFLVRFIKAAV   142

Qy   503  ANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISAYQRVIKVHVHVRTTD  562
            |:|:|:: ::  |  | |:  |  |:| | :|| :|| |:|  ::|  ||: :|||  :
Db   143  PDQELENMAHFMSELGMMNYAVLMYCPSMVAASAVFAARCTLNKAPLWNEFLKLHTGYSQ   202

Qy   563  NELPECVKSL  572
            :|:|:|:|
Db   203  EQLMDCARLL  212
```

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OX   NCBI_TaxID=6465;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Oocyte;
RX   MEDLINE=92007785; PubMed=1655419;
RA   van Loon A.E., Colas P., Goedemans H.J., Neant I., Dalbon P.,
RA   Guerrier P.;
RT   "The role of cyclins in the maturation of Patella vulgata oocytes.";
RL   EMBO J. 10:3343-3349(1991).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC       (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 AND CDK2 PROTEIN
CC       KINASES TO FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
CC       AND ARE ABRUPTLY DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN A/B SUBFAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X58357; CAA41254.1; -.
DR   PIR; S17792; S17792.
DR   HSSP; P20248; 1JSU.
DR   InterPro; IPR000553; Cyclin.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis.
SQ   SEQUENCE   426 AA;  48010 MW;  0A59O001E3162B37 CRC64;

Query Match             7.58;  Score 220;  DB 1;  Length 426;
Best Local Similarity   22.8%;  Pred. No. 2.4e-06;
Matches   109;  Conservative   74;  Mismatches   163;  Indels   132;  Gaps   17;

Qy   120  EKEGDEIEVSESSCCVDSNSGAGLRRLNVKGNKINDNDEISFSRSDVTFPAGHVSNSRSLNF  179
                 :| :|| ::|              |: |    |::  :: ::| | ::
Db    16  ENENQVQRVKKAGLIRARGNVAVAKRSALGTITNQNIRVQPSRA----------AKSGNADC   67

Qy   180  ESENKESDVVSVISGVEYCSKRGSSVTGGADNEIEISKPSSFEVEADSSLGSAKELKPELE  239
               |  :  | ||:  | :| |    :::    |:   || :   :::| :|::|| |
Db    68  QDENVFAKOKS------EGSSNNENKGFKIHVDEPTVQVLTTPATLKTTRQ-----       111

Qy   240  IVGCVSDLACSEKFSEEVSDSILDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGSEFSEK  299
                   |  | :| :|   | |  ::|   |:       |  :  |     :|:|  :|:|
Db   112  -----SEDEDIKILNDQVTSLPSLQALEDIQVDNENGSEPMV-LDVTIEDAEK         156

Qy   300  SSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSCEEIHSELLRFDDEEVEESYLRIRER   359
               :  |:|:|  :            | ::
Db   157  ----KPIDREAIIL------SVP-----                                   182

Qy   360  ERSH-----AYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQEIFLFLGVGLL  415
             |||         : |:|   :          ||::| || |: : ||::| :|:|| |::
Db   183  ESRHRSRPGYMK------KQPDITN--SMRSILVDMMVEVSEEYKLHRETLFLAINYI      232

Qy   416  DRFLSKGSFKSERTLILVGIASLITLATRIEENQP-----                       468
            ||||:   :| ||  :|||:||:| ||:   :: :
Db   233  DRFLSQMSVLRGK-LQLVGAASMFIASKYEEIYPPEVSEFVY-----              282

Qy   469  EVVAMEWLVQEVLNFKCFTPTIPNFLWFYLKAARANPEVERKAKSLA-----VTSLSDQT   523
             :: :|  :|:|  ||     | | ||:     |:|   | |: |       |||||::
Db   283  QVLRMEHLILKVLSFDVAQPTINWFTDTYAKMA-----DTDETTKSLSMYLSELTLVDADP  338

Qy   524  QLCFWPSTVAAALVVLACIEHN-----KISAYQRVIKVHVHVRTTDNELPECVKSL      572
             | ::||| |||:| | |::        |||| ::   | :    :|:| | |:
Db   339  YLKYLPSTIAAASLCLANITLGSSEPWPSSLAKESKYE-----ISEFSECLQEM         386

RESULT 9
```

ID   CGB2_RANJA   STANDARD;   PRT;   392 AA.
AC   O93229;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   G2/mitotic-specific cyclin B2.
GN   CCNB2.
OS   Rana japonica (Japanese reddish frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8402;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=99332197; PubMed=9669534;
RA   Ihara J., Yoshida N., Tanaka T., Mita K., Yamashita M.;
RT   "Either cyclin B1 or B2 is necessary and sufficient for inducing
RT   germinal vesicle breakdown during frog (Rana japonica) oocyte
RT   maturation.";
RL   Mol. Reprod. Dev. 50:499-509(1998).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC   (MITOSIS) TRANSITION.
CC   -!- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC   SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC   MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC   SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC   -!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC   ABRUPTLY DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC   --
CC   --
DR   EMBL; AB005253; BAA32563.1; -.
DR   HSSP; P20248; 1JSU.
DR   InterPro; IPR000553; Cyclin.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis.
SQ   SEQUENCE   392 AA; 43960 MW; 5038C4F851CC9C8 CRC64;

Query Match   7.4%; Score 217.5; DB 1; Length 392;
Best Local Similarity   28.6%;
  Matches   83; Conservative   44; Mismatches 102; Indels   61; Gaps   11;

Qy   315 QFKEQFCRSTIPNDFGSSSCEEEI-------HSELL-----------------RFDDEEVEESYLRLR 357
              |||| |
Db   82 QVKE---ASPVPMDVSMKEEEELCQAFSEVLNHVVDIDAEDGGNPOLCSEYVVDINYLR 138

Qy   358 ERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFGVGLLDR 417
Db   139 ERE----VQQSIKQRY---LDGMEINERMRAILVDWLIQVNSRFQFLQETLYMGIAIMDR 191

Qy   418 FL-------SKGSFKSERTLIIVGIASLTLATRIEIEENOPYNSIRKRNFT-IQNLRYSRHEVV 471
Db   192 FLQVQPISRGK----LQLVGVTSLLLASKYEE---MYSPEVADIFAYITDNAYTISQIR 242

Qy   472 AMEWLVQEVLNFKCFTPTIPNFLWFYLKAARANPEVERKAKSLAVTSLSDQTOLCFWPST 531
Db   243 EMEMILRELKFDLGRPLPHFLRRASKACSADAEOHTLARYLMEITLVDYEMVHFHPSE 302

Qy   532 VAAALVVLACIEIEHHKISAYQRVIKV---------HVRTTDNELPECVKSL 572
Db   303 IAAAAICLA-----------QKVLGVGSWGSTQHHYTGYTEEDLTPIIKHI 342

RESULT 10
ID   CGA2_XENLA   STANDARD;   PRT;   415 AA.
AC   P47827;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Cyclin A2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=95278730; PubMed=7758942;
RA   Howe J., Howell M., Hunt T., Newport J.;
RT   "Identification of a developmental timer regulating the stability of
RT   embryonic cyclin A and a new somatic A-type cyclin at gastrulation.";
RL   Genes Dev. 9:1164-1176(1995).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC   (START) AND THE G2/M (MITOSIS) TRANSITIONS.
CC   -!- SUBUNIT: INTERACTS WITH THE CDK2 AND CDC2 PROTEIN KINASES TO FORM
CC   A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC   IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC   -!- DEVELOPMENTAL STAGE: ACCUMULATE STEADILY DURING G2 AND IS ABRUPTLY
CC   DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC   --
CC   --
DR   EMBL; X87746; CAA59748.1; -.
DR   HSSP; P30274; 1VIN.
DR   InterPro; IPR000553; Cyclin.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis.
SQ   SEQUENCE   415 AA; 46670 MW; B0D530009A1764D CRC64;

Query Match   7.4%; Score 217.5; DB 1; Length 415;
Best Local Similarity   32.3%;
  Matches   76; Conservative   34; Mismatches   76; Indels   49; Gaps   9;

Qy   329 FGGSCCEEEIHSELLRFDDEE--------------VEESYLRLRERE----RSHAYMRDCAKAY 373
          |||| |
Db   136 FGGSPMDVSI------VDEEQKVVGCNNVADYAKEIHTYLREMEVCKPKRAGYMQ---- 183

Qy   374 CSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFGVGLLDRFLSKGSFKSERTLILV 433
Db   184 -KQPDITG---NMRAILVDWLVEVGEEYKLQNETLYLAVNYIDRFLSMSSVLRGK-LQLV 238

Qy   434 GIASLTLATRIEENOP-------YNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCF 486
Db   239 GTAAMLLASKFEEIYPPEVAEFVY------ITDDTVTKKQVLKMEHLVLKVLSFDLA 289

Qy   487 TPTIFNFLWFYLKAARANPEVERKRAKSLAVTSLSDQTQ-LCFWSTVAAALVVLLA 540
Db   290 APTILQYLNQYFQIHPVSRKVESLSMFLGELSLVDADPFLRYLPSVVAAAFVIA 344

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RESULT 11
ID   CG21_SOYBN     STANDARD;      PRT;   454 AA.
AC   P25011;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   G2/mitotic-specific cyclin S13-6 (B-like cyclin).
OS   Glycine max (Soybean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. AKISENGOKU; TISSUE=Root;
RX   MEDLINE=91330894; PubMed=1831125;
RA   Hata S., Kouchi H., Suzuka I., Ishii T.;
RL   "Isolation and characterization of cDNA clones for plant cyclins.";
RL   EMBO J. 10:2681-2688(1991).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC       (MITOSIS) TRANSITION.
CC   -!- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC       SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC       MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC       SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC   -!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC       ABRUPTLY DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
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CC   -------------------------------------------------------------------------
DR   EMBL; X62820; CAA44632.1; -.
DR   PIR; S15522; S15522.
DR   HSSP; P30274; 1VIN.
DR   InterPro; IPR000053; Cyclin.
DR   Pfam; PF00134; Cyclin; 1.
DR   Pfam; PF02984; Cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis.
SQ   SEQUENCE   454 AA;  50094 MW;  54EB4596586A7C10 CRC64;

Query Match             7.2%;
Best Local Similarity   21.5%;
Matches   95;  Conservative  91;  Mismatches 190;  Indels  66;  Gaps  17;

        Score 213; DB 1;  Length 454;
        Pred. No. 6.8e-06;

Qy  147 VKGNKINDNDEISFSRSDVTFAGHVSNSRSLNFESENKESDVVSISGVEYCSKFGSVTG 206
            ||      ||      |  |    |||||   | :: :     ||  ||
Db   17 VGGGKQOKKNGVADGRNKAL-GDIGNLANVRGVVDAKPNRPITRSFGAQLLAN-AQAAA 74

Qy  207 GADNEE----IEISKPSSFVEADSSLGSAKELKPELEIVGCVSDLACSEKFSEEVSDSLD 262
         :|| ||      | :| |   ||  :||:     | |  |  |  | |  :||:|
Db   75 AADNSKRQACANVAGPPAV---ANEGVAVAKRAAPK----PVSKKVIVKPKPSEKVTDI-- 126

Qy  263 DESSEQRSEIYSQYSDFD--------YSDYTPSIFFDSGSEFSEKSKSSSDSPISHSRSLYLQFK 317
         |  ::      :| |||         : |  | : |:| ||||||| ::|:||:||:|:| |
Db  127 DASPDKKEVLKDKKEGDANPRKKSQHLT-----SVLTARSKAACGITNKP-----K 174

Qy  318 EQFCRSTIPNDFGSSCEEEIHSELLRFD-DEEVEESYLRLRERERSHAYMRDCAKAYCSR 376
         || :   :     |: ||| || ||| | ||| ||: ||||  :  : | | |||| |
Db  175 EQII-----DIDAS--DVDNELAAVEYIDDIYKFYKLVENESRPHDYI--------- 215

Qy  377 MDNTGLIP----RLRSIMVQWIVKQCSDMGLQQETLFLGVGLLDREFLSKGSFKSERTLIL 432
          :  ||:|    || :: | |::  | |:| : | | ||: ||| ||:  || |:|  :|
Db  216 -----GSQPEINERMRAILVDWLLDVHHTKFELSLETLYLTINIIDRFLAVKTV-PRRELQL 270

RESULT 12
ID   CGA1_MOUSE     STANDARD;      PRT;   421 AA.
AC   Q61456;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Cyclin A1.
GN   CCNA1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=Testis;
RX   MEDLINE=99057346; PubMed=9843212;
RA   Liu D., Matzuk M.M., Sung W.K., Guo Q., Wang P., Wolgemuth D.J.;
RL   "Cyclin A1 is required for meiosis in the male mouse.";
RL   Nat. Genet. 20:377-380(1998).
RN   [2]
RP   ...
RX   MEDLINE=96152200; PubMed=8565853;
RA   Sweeney C., Murphy M., Kubelka M., Ravnik S.E., Hawkins C.F.,
RA   Wolgemuth D.J., Carrington M.;
RL   "A distinct cyclin A1 is expressed in germ cells in the mouse.";
RL   Development 122:53-64(1996).
CC   -!- FUNCTION.
CC   -!- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF THE CELL CYCLE AT THE
CC       G1/S (START) AND G2/M (MITOSIS) TRANSITIONS. MAY PRIMARILY
CC       FUNCTION IN THE CONTROL OF THE GERMLINE MEIOTIC CELL CYCLE AND
CC       ADDITIONALLY IN THE CONTROL OF MITOTIC CELL CYCLE IN SOME SOMATIC
CC       CELLS.
CC   -!- SUBUNIT: INTERACTS WITH THE CDK2 AND CDC2 PROTEIN KINASES TO FORM
CC       A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC       IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC   -!- SUBCELLULAR LOCATION: IN OOCYTES AT LEAST, IT ASSOCIATES WITH THE
CC       SPINDLE DURING METAPHASE.
CC   -!- TISSUE SPECIFICITY: TESTIS AND OVARIES.
CC   -!- DEVELOPMENTAL STAGE: IN MALE GERM CELLS JUST PRIOR TO OR DURING
CC       THE FIRST, BUT NOT THE SECOND MEIOTIC DIVISION.
CC   -!- MISCELLANEOUS: CCNA1 -/-MALES ARE STERILE DUE TO A BLOCK OF
CC       SPERMATOGENESIS BEFORE THE FIRST MEIOTIC DIVISION, WHEREAS FEMALES
CC       ARE NORMAL.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC   -------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Qy  433 VGIASLTLATRIEENQP--YNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTI 490
         ||::::: |::  |: :   ||:| :  ::  |||:|||| ||| : :|||||||| ||
Db  271 VGISAMLMASKYEEIWPPEVNDF----VCLLSDRAYTHEHILLTMEKTILNKLEWTLTVPTP 326

Qy  491 FNFLWFYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHHKISAY 550
         : :| :::|:  ||: :  :  |   ::  |  : : |||:|||:|||||:| | |:| |
Db  327 LVFLVRFIKASVPDQELDMAHFLSEIGMMNYATLMYCPSMVAASAVLAARCTLNKAPFW 386

Qy  551 QRVIKVHVRTDNELPECVKSL 572
          : :| | : ::|| :|  ||
Db  387 NETLKLHTGYSQEQLMDCARLL 408
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Left column

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CC   or send an email to license@isb-sib.ch).
CC   -----

DR   EMBL; X84311; CAA59053.1; -.
DR   HSSP; P30274; 1VIN.
DR   MGD; MGI:108042; Ccna1.
DR   InterPro; IPR000553; Cyclin.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 1.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis; Meiosis.
SQ   SEQUENCE 421 AA; 47712 MW; 7F701D00658D9BAD1 CRC64;

Query Match        7.2%; Score 212.5; DB 1; Length 421;
Best Local Similarity 27.2%; Pred. No. 6.6e-06;
Matches 92; Conservative 50; Mismatches 121; Indels 75; Gaps 14;

Qy  249 CSEKEFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGGSEFSEKSSSDSPISH 308
            :||  ||  ||  || ||:||:|:    |:|
Db  106 CSGKEGIIFEDVYEVDTSMLKSDLHFL---LDFNTVSPMLV-------DPTTH 148

Qy  309 SRSLYLQQFKEQFCRSTIPNDPGSSC------EEEIHSELLRFDDEEVEESYLRLRERERS 362
            :||   |||                                           |||
Db  149 AQS-----EE----ATDFGSDVINVTEYAEEIHRYL----PEAE-----VRHRPKA 186

Qy  363 HAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQEETLFLGVGLLLDRFLSKG 422
            |:|| |||:|:||:||  ||   || ||:||  ||||:|||||
Db  187 H-YMR------KQPDITEGMRAILVDWLVEVGEEYKLRTETLYLAVNFLDRFLSCM 235

Qy  423 SFKSERTLILVGIASILTLATRIEENQP------YNSIRKRNFTIQNLRYSRHEVVAMEW 475
            ||:|  |||||||||:||  |  |||:||   |||:||||| | |:  |:||
Db  236 SVLRGK-LQLVGTAAILLASKYEEIYPPDVDEFVY------ITDDTYTKROLLRMEH 285

Qy  476 LVQEVLNFKCFTPTTIPNFLWFYLKAARANPEVERKAKSLAVTSLSLSDQTQ-LCFWPSTVAA 534
            || |||||   |||| |:|||:|| |||||||  |: |  |
Db  286 LLKVLAFDLTVPTTNQFLLQYLRRQCVCIRTENLAKYVAELSLLEADPFLKYLPSLVAA 345

Qy  535 ALVVLACIEIHNKISAYQRVIKVHVRTTDNELPECVKSL 572
            |: ||  |||
Db  346 AAYCLANYIVNR-HFWPETLAAFTGYSLNEIVPCLSEL 382
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RESULT 13
CG2A_SPISO

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ID   CG2A_SPISO     STANDARD;      PRT;   422 AA.
AC   P04962;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   G2/mitotic-specific cyclin A.
OS   Spisula solidissima (Atlantic surf-clam).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
OC   Mactroidea; Mactridae; Spisula.
OX   NCBI_TaxID=6584;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87051767; PubMed=2946420;
RA   Swenson K.I., Farrell K.M., Ruderman J.V.;
RT   "The clam embryo protein cyclin A induces entry into M phase and the
RT   resumption of meiosis in Xenopus oocytes.";
RL   Cell 47:861-870(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9109664; PubMed=2148535;
RA   Standart N., Dale M., Stewart E., Hunt T.;
RT   "Maternal mRNA from clam oocytes can be specifically unmasked in
RT   vitro by antisense RNA complementary to the 3'-untranslated region.";
RL   Genes Dev. 4:2157-2168(1990).
CC   -|- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC   (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 AND CDK2 PROTEIN
CC   KINASES TO FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
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Right column

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CC   AND ARE ABRUPTLY DESTROYED AT MITOSIS.
CC   -|- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC   -----
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DR   EMBL; M14535; AAA98921.1; -.
DR   EMBL; X55127; CAA38921.1; -.
DR   HSSP; P30274; 1VIN.
DR   InterPro; IPR000553; Cyclin.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 1.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis.
SQ   SEQUENCE 422 AA; 47777 MW; C6C003303A1267F CRC64;

Query Match        7.2%; Score 212; DB 1; Length 422;
Best Local Similarity 26.3%; Pred. No. 7.1e-06;
Matches 108; Conservative 54; Mismatches 155; Indels 94; Gaps 17;

Qy  136 SNSGAGLRR--LNVKGNKINDNDEIISFRSDVTFAGHVSNSRSLNFESENKESDVVSVIS 193
            ||| |:||
Db   25 SNGLSGQKRAALGVITNQVNQQVRIQPSRA----AKPKSSEFNIQDENA------- 69

Qy  194 GVEYCSKFGSVTGGADNEEIEISKPSSF-VEADSSLGSAKELKPELEIVGCVSDLACSEK 252
            | |:|| | |                      |:|:
Db   70 ----FTKKNAKTFG------QQPSQFSVFVDPTPPAAPVQKAPTSHVTDIPAALTTLQR 117

Qy  253 FS-EEVSDSLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGGSEFSEKSSSDSPISHSRS 311
            || ||:|||                   :|:
Db  118 VPLTEVPGSPFDIISLEDSME----------SPMIL-----DLPEEEKPLDREAV 156

Qy  312 LYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRFDDEEVEESYLRLRERERSHAYMRDCAK 371
            |:|   |                                             ||:
Db  157 LL----TVP----EYEEDIY----NYLR------QAEMKNRAK 181

Qy  372 -AYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQEETLFLGVGLLLDRFLSKGSFKSERTL 430
             ||:|:||:||  || ||:||  ||||:|||||   |||||| |::||||||||:|:||||
Db  182 PGYMKR--QTDITTSMRCILVDWLVEVSEEDKLHRETLFLGVNYIDRFLSKISVLRGK-L 238

Qy  431 ILVGIASILTLATRIEENQPYNSIRKRNFTIQNLRYSRHEVVAMENLVQEVLNFKCFTPTI 490
            ||||||:||| |  |||:||                 |:  |:||
Db  239 QLVGAASMFLAAKYEEIYPPDV--KEFAYITDDTYTSQQVLRMEHLILKVLTFDVAVPTT 296

Qy  491 FNFLWFYLKAARANPEVERKAKSLAVTSLSD-QTQLCFWPSTVAAALVVLA 540
            |||||:||   |||
Db  297 NWFCEDFLKSCDADDKLKSLTMFLTELTLILDMDAYLKYLPSITAAAALCLA 347
```

RESULT 14
CGA2_MESAU

```
ID   CGA2_MESAU     STANDARD;      PRT;   421 AA.
AC   P37881;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Cyclin A2 (Cyclin A).
GN   CCNA2 OR CCNA.
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RA   Shiraki T., Yamashita K., Nishitani H., Nishimoto T.;
RL   Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC       (START) AND THE G2/M (MITOSIS) TRANSITIONS.
CC   -!- SUBUNIT: INTERACTS WITH THE CDK2 AND CDC2 PROTEIN KINASES TO FORM
CC       A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC       IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC   -!- DEVELOPMENTAL STAGE: ACCUMULATE STEADILY DURING G2 AND IS ABRUPTLY
CC       DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC   ---
```
```
DR   EMBL; D17295; BAA04128.1; -.
DR   HSSP; P20248; 1JSU.
DR   InterPro; IPR000553; Cyclin.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis.
SQ   SEQUENCE 421 AA; 47327 MW; F57J6C97D62667CD CRC64;

Query Match    7.1%; Score 211; DB 1; Length 421;
Best Local Similarity   23.3%;
Matches   95; Conservative   68; Mismatches 147; Indels   98; Gaps   13;

Qy  168 AGHVSNSRSLNFESSENKESDVVSVISGVEYCSKEGSVTGGADNEEIEISKPSSFVEADSS 227
Db    8 SGREAGSALLSLQQEDQE--------------------NVNPEKAAPDQRARAALK 43

Qy  228 LGSAKELKPELEI------VGCVSDLACSEKF------SEEVSDSLDDESSEQRSEIY 273
Db   44 TGNARGNAPQQRLKARRVAPLKDLSINDEHVASGPSWKAASKQPAFTIHVDEEEDTQKIP 103

Qy  274 SQYSDFDYSDYTPSIFFDSG------------SEFSEKSSSDSPISHSRSLYLQFKEQFC 321
Db  104 PEHKEMRCED---ALAFNAAVSLPGARKPLVPLDIPMDGSFESPHAMDMSIVLEEEKPVS 160

Qy  322 RSTIPNDFGSSCEEEIHSELLRFDDEEVEESYLRLRERERSHAYMRDCAKAYCSRMDNTG 381
Db  161 VNEVPD-----YHEDIH------------TYLREMEIK---------CKPKVGYMKQPD 194

Qy  382 LIPRLRSIMVQWIVKQCSDMGLQQEETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLA 441
Db  195 ITNSMRAILVDWLVEVGEEYKLQNETLHLAVNYIDRFLSSMSVLRGK-LOLVGTAAMLLA 253

Qy  442 TRIEENQP--------YNSIRKRNFTIQNLRYSRHEVVANEMFLVQEVLNFKCFTPFIFNFL 494
Db  254 SKFEEIYPPEVAEFVY---ITDDTYSKKQVLRMEHLIVLKVLAFDLAAPFVNQFL 304

Qy  495 -WFYLKAARANPEVERKAKSLAVTSLSD--QTQLCFWPSTVAAALVVLA 540
Db  305 NQYFLHQQPANCKVESLAMFLGELSLIDADPYLKYLPSLIAGAAFHLA 352


RESULT 15
CGA2_BOVIN
ID   CGA2_BOVIN    STANDARD;    PRT;    406 AA.
AC   P30274;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Cyclin A2 (Cyclin A) (Fragment).
GN   CCNA2 OR CCNA.
```

```
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocytes;
RX   MEDLINE=93091274; PubMed=1333843;
RA   Kobayashi H., Stewart E., Poon R., Adamczewski J.P., Gannon J.,
RA   Hunt T.;
RL   Mol. Biol. Cell 3:1279-1294(1992).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 155-406.
RX   MEDLINE=96164440; PubMed=8591034;
RA   Brown N.R., Noble M.E.M., Endicott J.A., Garman E.F., Wakatsuki S.,
RA   Mitchell E., Rasmussen B., Hunt T., Johnson L.N.;
RT   "The crystal structure of cyclin A.";
RL   Structure 3:1235-1247(1995).
CC   -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC       (START) AND THE G2/M (MITOSIS) TRANSITIONS.
CC   -!- SUBUNIT: INTERACTS WITH THE CDK2 AND CDC2 PROTEIN KINASES TO FORM
CC       A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC       IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC   -!- DEVELOPMENTAL STAGE: ACCUMULATE STEADILY DURING G2 AND IS ABRUPTLY
CC       DESTROYED AT MITOSIS.
CC   -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC       "identification of the domains in cyclin A required for binding to,
CC       and activation of, p34cdc2 and p33cdk2 protein kinase subunits.";
CC   ---
```
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DR   EMBL; X68321; CAA48398.1; -.
DR   PIR; S24788; S24788.
DR   PDB; 1VIN; 17-AUG-96.
DR   InterPro; IPR000553; Cyclin.
DR   Pfam; PF00134; cyclin; 1.
DR   Pfam; PF02984; cyclin_C; 1.
DR   SMART; SM00385; CYCLIN; 2.
DR   PROSITE; PS00292; CYCLINS; 1.
KW   Cyclin; Cell cycle; Cell division; Mitosis; 3D-structure.
FT   NON_TER      1      1
SQ   SEQUENCE 406 AA; 45968 MW; 8280DAC125DB65B0 CRC64;

Query Match    7.1%; Score 210.5; DB 1; Length 406;
Best Local Similarity   24.9%;
Matches   93; Conservative   65; Mismatches 134; Indels   81; Gaps   13;

Qy  209 DNEEIEISKPS------------SPVEADSSLGSAKELKPELEIVGCVSDLACSEKF---- 253
Db    5 DQENVNPEKAAPAQQPRTRAGLAVLRAGNSRGPAPQ-RPKTRRVAPLKDLPINDEYVPVP 63

Qy  254 -----SEEVSDSLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSG------------SEF 296
Db   64 PWKANNKQPAFTIHVDEAE---EIQKRPTESKKSESEDVLAFNSAVTLPGPRKPLAPLDY 120

Qy  297 SEKSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRFDDEEVEESYLRL 356
Db  121 PMDGSFESPHTMEMSVVLEDEKPVSVNEVPD-----------YHEDIH----- 162

Qy  357 RERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQEETLFLGVGLLD 416
Db  163 MEVK-----------CKPKVGYMKQPDITNSMRAILVDWLVEVGEEYKLQNETLHLAVNYID 214

Qy  417 RFLSKGSFKSERTLILVGIASLTLATRIEENQP-------YNSIRKRNFTIQNLRYSRHE 469
```

```
Db  215 RFLSSMSVLRGK-LQLVGTAAMLLASKFEEIYPPEVAEFVY----------ITDDTYTKKQ 264
Qy  470 VVAMEWLVQEVLNFKCFTPTIFNFL-WFYLKAARANPEVERKAKSLAVTSLSD-QTQLCF 527
            |:||  | |||  :||     |||   || |    |  :
Db  265 VLRMEHLVLKVLAFDLAAPTINQFLTQYFLHQQPANCKVESLAMFLGELSLLIDADPYLKY 324

Qy  528 WPSTVAAALVVLA 540
            || :||| ||
Db  325 LPSVIAAAFHLA 337
```

Search completed: July 23, 2002, 14:26:22
Job time: 236 sec

```
OM protein - protein search, using sw model

                            GenCore version 4.5
                            Copyright (c) 1993 - 2000 Compugen Ltd.

Run on:           July 23, 2002, 14:18:56 ; Search time 20.95 Seconds
                            (without alignments)
                            2651.057 Million cell updates/sec

Scoring table:

Sequence:         1 MKEIAMRNSRKPEPPFAG.........RTTDNELPECVKSLDWILGQ 578
Perfect score:    2952
Title:            US-09-821-839-2

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:        283138

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        PIR_71:*
                  1:  pir1:*
                  2:  pir2:*
                  3:  pir3:*
                  4:  pir4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match Length	% Match	DB ID	Description
1	281.5	429	2	T04667	cyclin 2b - Arabid
2	262.5	434	2	V97706	cyclin cycMs2, B-t
3	252.5	328	2	S29925	cyclin 2 - alfalfa
4	250	428	2	S56679	mitosis-specific c
5	242.5	452	2	S95596	cyclin cyc3 - alfa
6	241	424	2	D57742	cyclin cyc3 - alfa
7	239.5	429	2	D84554	cyclin III - maize
8	236.5	454	2	T10526	probable cyclin 2
9	234.5	445	2	S65734	cyclin B1b-l1 - ye
10	233.5	419	2	T03675	mitosis-specific c
11	233	460	2	B86339	cyclin 2 - rice
12	232.5	446	2	T03021	protein F2D10.10 1
13	229	452	2	T10527	cyclin B1d-l1 - ye
14	227.5	341	2	S16521	mitosis-specific c
15	227.5	454	2	A96803	probable mitotic c
16	227	456	2	C57742	cyclin II - maize
17	225	459	2	T10526	cyclin B1c-l1 - ye
18	223.5	473	2	S41709	mitosis-specific c
19	223	502	2	T02746	cyclin A-like prot
20	222.5	257	2	S74673	mitosis-specific c
21	222.5	418	2	F96790	hypothetical prote
22	222	473	2	T03611	cyclin B-type - c
23	220	426	2	S17792	cyclin A - common
24	219.5	483	2	T02966	cyclin A-type (clo
25	218.5	483	2	T03606	cyclin, A-type - c
26	217.5	483	2	I51637	cyclin A2 - Africa
27	215	443	2	T14916	mitosis-specific c
28	215	482	2	T02967	cyclin A-type (clo
29	214	493	2	T03609	cyclin, A-type - c
30	213.5	469	2	T07672	cyclin a2-type, m1
31	213	454	2	S16522	mitosis-specific c
32	212	422	2	A26328	cyclin A - Atlanti
33	210.5	406	2	S24788	cyclin A - bovine
34	209.5	440	2	T07676	cyclin b1-type, m1
35	209	484	2	T07675	cyclin a2-type, mi
36	209	418	2	S11678	cyclin a2-type, mi
37	207.5	242	2	S49462	cyclin A - African
38	207.5	432	2	S08277	cyclin A - rice
39	207.5	461	2	D96835	probable cyclin, 4
40	206	430	2	A43285	cyclin A - human
41	204.5	384	2	T02968	cyclin A-type (clo
42	204.5	460	2	D96505	probable mitotic c
43	204	430	2	I48316	cyclin B1 - mouse
44	202.5	348	2	T07669	cyclin a1-type, ml
45	202	441	2	S41710	mitosis-specific c

ALIGNMENTS

```
RESULT    1
T04667
cyclin 2b - Arabidopsis thaliana
N;Alternate names: protein F8D20.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-May-1999
C;Accession: T04667
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mew
  submitted to the Protein Sequence Database, July 1998
A;Cross-references: EMBL:AL031135
A;Experimental source: cultivar Columbia; BAC clone F8D20
C;Genetics:
A;Reference number: Z15381
A;Accession: T04667
A;Molecule type: DNA
A;Residues: 1-429 <BEV>
A;Note: F8D20.130
A;Map position: 4
A;Introns: 22/1; 67/2; 87/2; 138/3; 184/3; 214/3; 288/3; 321/3; 381/2
C;Superfamily: cyclin
C;Keywords: cell cycle control; cell division control; mitosis
```

```
Query Match             9.5%;   Score 281.5; DB 2;   Length 429;
Best Local Similarity   27.3%;  Pred. No. 3.6e-10;
Matches   94; Conservative  69; Mismatches  134; Indels   47; Gaps   13;

Qy    248 ACSEKFSEEVSDSLDDESSEQRSIIYSQYSFDYSDYTPSIFFDSGSSERSEKSSSDSPIS 307
          ::|: ||  :|||||||   |:|||||||   ||:||||  | ||:| ||:|||:| :||:
Db     72 SCDKKKLDSLHPSI-SRSQQETKKLKPSGGNEFG-----DCIFIDEEEEKNEEVTLDQPMP 125

Qy    308 HS-RSLYLQFKEQFCRSTIFNDFGSSCEEIHSELLRFDDEEVEESYLRLRERERSHA-- 364
          |:|        |:|||||||||||||||||||: |:|||||| :::||:||||||||
Db    126 MSLEEPYIEF-----------------DPMEEEVEMDM--EEEQEEPVLDIDEYDANNSLA 168

Qy    365 --YMRDCAKAY-----------CSRMD-----NTGLIPRLRSIMVQWIVKQCSDMGLQQETLFL 410
          :  |::|        |:|:|   :|:|:::||  ||| || |:| |:
Db    169 AVEEVQDLYDFYRKTERFSCVPLDYMAQQFDISDKMRAILIDWLLIEVHDKFELMNETLFL 228

Qy    411 GVGLLDRFLSKGSFKSERFLILVGIASLTLATRIEE-NQPYNSIRKRNFTIQNLRYSRHE 469
          :|: ||:|||||  | ||||||||:|||:|| | | ||:  |:|| | ||:|  |:|||
Db    229 TVNLIDRFLSKQAV-ARKKLQLVGLVALLLACKYEEVSVP----IVEDLVVISDKAYTRTD 284

Qy    470 VVAMEWLVQEVLNEKCFTPPIFNELWFYLKAARANPEVERKAKSLAVTSLSDQTQLCFWP 529
          |:| |:|||::|: |:| | |||:|| |: |  |:|::||:|:|:|::|:::| |
Db    285 VLEMEKIMLSTLQFNMSLPTQYPFLKRFLKAAQSDKLEILASFLELALVDYEMVRYPP 344

Qy    530 STVAAALVVLA-CIEHNKISAYQRVIKVHVRTTDNELPECVKSL 572
          ||:|| |:| |||: |::| | | ||::||:||: |||| |
Db    345 SLLAATAVYTAQCTIHG-FSEWNSTCEFHCHYSENQLLECCRRM 387
```

RESULT 2
T09706
C;Species: Medicago sativa (alfalfa)
C;cyclin cycMs2, B-type - alfalfa
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
C;Accession: T09706
R;Meskiene, I.; Boegre, L.; Dahl, M.; Pirck, M.; Ha, D.T.C.; Swoboda, I.; Heberle-Bors,
Plant Cell 7, 759-771, 1995
A;Title: CycMs3, a novel B-type Alfalfa cyclin gene is induced in the G0-to-G1 transitio
A;Reference number: Z16831; MUID:95375541
A;Accession: T09706
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-434 <MES>
A;Cross-references: EMBL:X82040; NID:g914862; PID:g914863
A;Experimental source: subspecies A2
C;Superfamily: cycMs2
C;Genetics:
C;Gene: cycMs2
C;Keywords: cell cycle control; cell division control; mitosis

Query Match   8.9%; Score 262.5; DB 2; Length 434;
Best Local Similarity 27.0%; Pred. No. 5.6e-09;
Matches   86; Conservative   57; Mismatches 112; Indels   63; Gaps   8;

Qy   292 SGSEFSEKSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSC------------------- 333
          : |||| ::|:|||
Db   92 SQQSYAEKTKNSNPLN-----------------LNEFGNSIAIDDELKSPEDQPEPMTL 133

Qy   334 --EEIHSELLRFDDEEVEE--------------SYLRLRERERSHAYMRDCAKAYC--- 374
          ||:|||| ||||||||:||
Db   134 EHTEPMHSDPLEMEEVEMEDIEGEMILDIDSCDANNSLAVVEYIEDLHAYYRKIEYLGCV 193

Qy   375 --SRMD-NTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLI 431
          | ||| |||||||| |||||| |||||||||||||||||||
Db   194 SPTYMDEQLDLNERMRAILVDWLIEVHDKFDLMQETLFLTVNLIDRFLAKQNVVRKK-LQ 252

Qy   432 LVGIASLTLATRIEE-NQPYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTI 490
          |||||||||||||| ||||||||||| ||||||||||||||||||||||||||:|||
Db   253 LVGLVAMLLACKYEEVSVP---VVSDLIHIADRAYTRKDILEMEKLMLNTLQYNMSLPTA 309

Qy   491 FNFLWFYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISAY 550
          |||||||||||||||||||||||||||| ||:||||||||||| :||||||:
Db   310 YVFMRRFLKAAQADRKLELVAFFLVDLSLVEYEMLKFPPSLVAAAAVYTAQCTVSGFKHW 369

Qy   551 QRVIKVHVRTDNELPEC 568
          |||||||||||||||||
Db   370 NKTCEWHTNYSEDQLLEC 387

RESULT 3
S29925
C;cyclin 2 - alfalfa (fragment)
C;Species: Medicago sativa (alfalfa)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C;Accession: PQ0490; S29925
R;Hirt, H.; Mink, M.; Pfosser, M.; Boegre, L.; Gyoergyey, J.; Jonak, C.; Gartner, A.; Du
Plant Cell 4, 1531-1538, 1992
A;Title: Alfalfa cyclins: differential expression during the cell cycle and in plant org
A;Reference number: PQ0489; PQ0490
A;Accession: PQ0490
A;Molecule type: mRNA
A;Residues: 1-328 <HI2>
A;Cross-references: GB:X68741; NID:g19598; PIDN:CAA48675.1; PID:g19599
C;Comment: This protein is a type B cyclin.
C;Genetics:
C;Gene: cycMs2
C;Superfamily: cyclin

Query Match   8.6%; Score 252.5; DB 2; Length 328;
Best Local Similarity 30.6%; Pred. No. 1.6e-08;

Matches   78; Conservative   48; Mismatches 104; Indels   25; Gaps   6;

Qy   335 EEIHSELLRFDDEEVEE----------------SYLRLRERERSHAYMRDCAKAYC---S 375
          ||:||||||||||||| ||||||||||||||||||||| |
Db   31 EPMHSDPLEMEEVEMEDIEGEMILDIDSCDANNSLAVVEYIEDLHAYYRKIEYLGCVSPT 90

Qy   376 RMD-NTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVG 434
          ||| |||||||| |||||| |||||||||||||||||||||||||
Db   91 YMDEQLDLNERMRAILVDWLIEVHDKFDLMQETLFLTVNLIDRFLAKQNVVRKK-LQLVG 149

Qy   435 IASLTLATRIEE-NQPYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNF 493
          |||||||||| ||||||||||| |||||||||||||||||||||||:||||
Db   150 LVAMLLACKYEEVSVP---VVSDLIHIADRAYTRKDILEMEKLMLNTLQYNMSLPTAYVF 206

Qy   494 LWFYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISAYQRV 553
          | |||||||||||||||||||| ||:||||||||||||| :|||||:
Db   207 MRRFLKAAQADRKLELVAFFLVDLSLVEYEMLKFPPSLVAAAAVYTAQCTVSGFKHWNKT 266

Qy   554 IKVHVRTDNELPEC 568
          |||||||||||||
Db   267 CEWHTNYSEDQLLEC 281

RESULT 4
S56679
C;mitosis-specific cyclin CycIII - alfalfa
N;Alternate names: B3-type mitotic cyclin; group III cyclin
C;Species: Medicago sativa (alfalfa)
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
C;Accession: S56679
R;Savoure, A.; Feher, A.; Kalo, P.; Petrovics, G.; Csanadi, G.; Szecsi, J.; Kiss, G.;
Plant Mol. Biol. 27, 1059-1070, 1995
A;Title: Isolation of a full-length mitotic cyclin cDNA clone CycIIIMs from Medicago
A;Reference number: S56679; MUID:95284356
A;Accession: S56679
A;Molecule type: mRNA
A;Residues: 1-428 <SAV>
A;Cross-references: EMBL:X78504; NID:g780266; PIDN:CAA55272.1; PID:g780267
A;Experimental source: Medicago sativa ssp. sativa cv. Sitel
C;Superfamily: cyclin
C;Keywords: cell cycle control; cell division control; mitosis
F;29-37/Region: destruction motif

Query Match   8.5%; Score 250; DB 2; Length 428;
Best Local Similarity 25.8%; Pred. No. 3.3e-08;
Matches   90; Conservative   68; Mismatches 121; Indels   70; Gaps   13;

Qy   250 SEKFSEEVSD--SLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGGSEFSEKSSSDSPIS 307
          ::||:| :| :||::|| ||:: |:: : ||| :|| ::
Db   75 TRRFAAKIANTKTTNAEGTIKRSNL-AKSSSNGFGDF---IFVDD----EHKPVEDQPVP 126

Qy   308 HSRSLYLQFKEQFCRSTIPNDFGSSGCEEEIHSELLRFDDEEVEE------------S 352
          |:: |:|| || : ||| | ::||| |:|||||||||||
Db   127 MA-----LEQ-------TEPMHSESDRMEEVEMEDIMEEPVMDIDTPDAND-----S 165

Qy   353 YLRLRERERSHAYMRDCAKAYCSRMDNTGLI------------PRLRSIMVQWIVKQCSD 400
          ||||||||||||||||| |:::||||||| |||||||||||||||||
Db   166 PLAVAE------YIED-LYSYRKVESTSCVSPNYMAQQFDLNERMRAILVDWLIEVHDK 218

Qy   401 MGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEE--NQPYNSIRKRNFT 459
          |||||||||||||||||||||||||||||||| ||||||||||| |||||||||||
Db   219 FDLMHETLFLTVNLIDRFLEKQSVVRKK-LQLVGLVAMLLACKYEEVSVPRAYVFMRRFLKA 274

Qy   460 IQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTSL 519
          : ||||| ||||||||||:||||: :| |||||||||||||||||||:
Db   275 ISDRAYTRKEVLEMEKVMVNALKFNISVPRAYVFMRRFLKAAQADRKLELVAFFLIELSL 334

Qy   520 SDQTQLCFWPSTVAAALVVLACIEHNKISAYQRVIKVHVRTDNELPEC 568
          ||:||||||||||| :|||||:
Db   335 VEYAMLKFSPSQLAAAAVYTAQCTMYGVKQWSKTCEWHTNYSEDQLLEC 383

Qy   554 IKVHVRTDNELPEC 568
          |||||||||||||
Db   267 CEWHINYSEDQLLEC 281

RESULT 5

```
T09596
cyclin cyc3 - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C;Accession: T09596
R;Meskiene, I.
submitted to the EMBL Data Library, November 1995
A;Reference number: 216758
A;Accession: T09596
A;Molecule type: mRNA
A;Residues: 1-452 <MES>
A;Cross-references: EMBL:X85783; NID:g1071696
C;Genetics:
A;Gene: cycMs3
A;Superfamily: cyclin
```

```
Query Match       8.2%;  Score 242.5;  DB 2;  Length 452;
Best Local Similarity  27.0%;  Pred. No. 1e-07;
Matches 110;  Conservative 68;  Mismatches 148;  Indels 81;  Gaps 15;
```

```
Qy  163 SDVTPAGH------------VSNSRSLNFESENKESDVVSVISGVEYCSKFGPSVTGGADNEEIE 214
Db   24 SDVTYLPHKKRAILQDVTNNCGVNTKR------SCLNPTEIQAK-------KRK 64

Qy  215 ISKPSSFVEADSSLGSAKELKPELEIVGCVSDLACSEKFSEEVS--DSLDDESSEQRSEI 272
Db   65 VAKPAQ-PHVSNEVPSAAELPPIADSKPVSSMEMRLRSSEDFRCLLDDLEDNAPFRMSS- 122

Qy  273 YSQYSDFDYSDYTPSIFFDSGSSEFSEKSSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSS 332
Db  123 ------NQCGTNNNLLQSQTSRIS-ARPLSSQKKASQIVAAKKGNISEL 164

Qy  333 CEEEIHSEL-----LRFDDEEVEESY                                    380
Db  165 LDVSKIPDVADIDADEDPQLCSHYAADIYDHLRVAELSR------RPYPNFMETVQ 215

Qy  381 -GLIPLRSIMYQWIVKQCSDMGLQQEETLFLGVGLLDRFLSKGSFKSERTLILVGIASLT 439
Db  216 QDITPSMRAILVDWLVEVSEGYKLQANTLSLTVYLIDWFLSKNCIERER-LQLLGITCML 274

Qy  440 LATRIEENQPYNSIRKRNFT-IQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLMFYL 498
Db  275 IATKYEE---INAPRIKDFCFIQDNTYTKEEVVKLESLVLKSSSYQLFAPTTKTFLRRFL 331

Qy  499 KAARA-----NPEVERRAKSLAVTSLSDQTLCFWPSTVAAALVVLA 540
Db  332 RAAQASYRPSIELEYLANYLAELTLMNYGFLNFLPSMVAASSVFLA 378
```

RESULT 6

```
D57742
cyclin III - maize
C;Species: Zea mays (maize)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 16-Jul-1999
C;Accession: D57742
R;Renaudin, J.P.; Colasanti, J.; Rime, H.; Yuan, Z.; Sundaresan, V.
Proc. Natl. Acad. Sci. U.S.A. 91, 7375-7379, 1994
A;Title: Cloning of four cyclins from maize indicates that higher plants have three stru
A;Reference number: A57742; MUID:94316698
A;Accession: D57742
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-424 <REN>
A;Cross-references: GB:U10076; NID:g516547; PIDN:AAA20236.1; PID:g516548; GB:U10077; GB:
C;Superfamily: cyclin
```

```
Query Match       8.2%;  Score 241;  DB 2;  Length 424;
Best Local Similarity  21.9%;  Pred. No. 1.2e-07;
Matches 94;  Conservative 92;  Mismatches 162;  Indels 82;  Gaps 15;
```

RESULT 7

```
D84554
probable cyclin 2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: D84554
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Shen, M.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: D84554
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-429 <STO>
A;Cross-references: GB:AE002093; NID:g4926869; PIDN:AAD32949.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g17620
A;Map position: 2
C;Superfamily: cyclin
```

```
Query Match       8.1%;  Score 239.5;  DB 2;  Length 429;
Best Local Similarity  24.9%;  Pred. No. 1.5e-07;
Matches 91;  Conservative 70;  Mismatches 155;  Indels 49;  Gaps 9;
```

```
Qy  178 NFESENKESDVVSVISGVEYC------------SKFGSVTGGADNEEIEISKPS-SPVEAD 225
Db    3 NLRSQNCHQGV-AMEGVKFAPEKANTNRRALSDIKNIIGG-PHQHLAVSKRALSEKPAA 59

Qy  226 SSLGSAKELKPELEIVGCVSDLACSEKFSEEVSDS----LDDESSEQRSEIYSQYSDFD 280
Db   60 AAAAANAKDQ------AGFVGHRPVTRKFAAATLATQPTVALLDPIGSERLKR----NAD 107

Qy  281 YSDYTPSIFFDSGSSEFSEKSSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSS 340
Db  108 TAFHTPA------DMESTKMTDDSPL-------PMVSEMDEMMSPE 140

Qy  341 LLRFDDEEVEESYLRLRERERSHA------YMRDCAKAYCSRMDNTGLIP------ 384
Db  141 LKEIEMEDIEEAAPDIDSGDAGNSLAVADYVDEIYRFY-RKTEGASCVPTNYMSSQTDIN 199

Qy  385 -RLRSIMYQWIVKQCSDMGLQQEETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTIATR 443
Db  200 EKMRGILIIDWLIEVHYKLELLEETLFLTVNIDRFLARENVVRKK-LQLAGVTAMLLACK 258

Qy  444 IEE-NQPYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLMFYLKAAR 502
Db  259 YEEVSVP---VVEDLILICDRAYTRADILEMERRIVNTILNFNMSVPPYCEMRRFLKAAQ 315

Qy  503 ANPEVERRAKSLAVTSLSDQTLCFWPSTVAAALVVLACIEIENKISAYQRVIKVHVRTTD 562
Db  316 SEKKLELLSFFMIELSLVEYEMLQFCPSMLAAAAIYTAQCTINGFKSWNKCCELHTRYSE 375

Qy  563 NELPECVKSL 572
Db  376 EHLMVCSRMM 385
```

```
Qy  222 VEADSSLGSAKELKPELEIVGCVSDLACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDY 281
Db   57 VNKRGSLLSNKQEBEE------GCQKKKFDSLRPSVTRSGVEEETNKKLKPSVPSA 106

Qy  282 SDYTPSIFFDSGSSEFSEKSSSSDSPISHS--RSLYLQFKEQFCRSTIPNDFGSS 340
Db  107 NDEGDCIFID----EEEATLDLPMPMSLEKPYIE------ADPMEVEME 146

Qy  341 LLRFDDEEVEESYLRLRERERSHAYMRDCAKAYCSRMDNTGLIP-------RLRS 388
Db  147 DVTVEEPIVDIDVLDSKNSLAAVEYVQD-LYAFYRTMERFSCVPVDYMMQQIDLNEKMRA 205

Qy  389 IMYQWIVKQCSDMGLQQEETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEE-N 447
```

RESULT 8

```
T10525
cyclin B1b-11 - yellow lupine
C;Species: Lupinus luteus (yellow lupine)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T10525
R;Deckert, J.; Jelenska, J.; Zaborowska, Z.; Legocki, A.B.
   Acta Biochim. Pol. 44, 37-42, 1997
A;Title: Isolation and classification of a family of cyclin gene homologues in Lupinus l...
A;Reference number: Z17072; MUID:97385338
A;Accession: T10525
A;Molecule type: mRNA
A;Status: translated from GB/EMBL/DDBJ
A;Accession: T10525
A;Residues: 1-454 <DEC>
A;Cross-references: EMBL:U24193; NID:g3253134; PIDN:AAC61888.1; PID:g3253135
A;Experimental source: clone CycB1b-11
A;Superfamily: cyclin
C;Keywords: cell cycle control; cell division control; mitosis
```

Query Match 8.0%; Score 236.5; DB 2; Length 454;
Best Local Similarity 22.7%; Pred. No. 2.5e-07;
Matches 97; Conservative 71; Mismatches 189; Indels 71; Gaps 11;

```
Qy  147 VKGNKINDNDEISFSRSDVTFAGHVSNSRSLNFESENKESDVVSVISGVEYCSKFGSVTG  206
Db   50 VKGANINLNRPITRSLCAQLLAKAEAGENDKNLAIPNVTGPKPQVADGV--VAKRRVAPK  107

Qy  207 GADNEEIEISKPSSPVEADSSLGSARELKPELEIVGCVSDLACSEKFSEEVSDSLDDESS  266
Db  108 PAEKKVTAKPVEIVE---ISSGKEVQKDK--------SANNKEQQDALSKKKS         152

Qy  267 EQRSEIYSQYSDFDYSDYTPSIFFDSGGSEFSEKSSSDSPISHSRSLYLQFKEQFCRSTIP 326
Db  153 QTLYSVLTARS-----------------------KAACGLTEKP------ID          179

Qy  327 NDFGGSCEEIHSELLRFDDEDEVEESYLRLRERERSHAYMRDCAKAYCSRMDNTGLIPRL  386
Db  180 IDAGDSRNELAAVEYI----EDMYKFYKLAENENRPHQYMD------SOPEINERM      225

Qy  387 RSIMYQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEE  446
Db  226 RAILVDWLIDVQTKFDLSLEFLYLTINIVDRFLAVKIV-LRRELQLVGVSAMLMASKYEE  284

Qy  447 NQP--YNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARAN  504
Db  285 IWPPEVNDF---VCLTDRAYTHEQLLVMERKILGKLEWTLTVPFTFVFLIRFIKASVPD   340

Qy  505 PEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISAYQRVIKVHVRRTTDNE 564
Db  341 QELENMGHFLSELGMMHYATLVYCPSMVAASAVFAARCTLNKTPIWNETLQLHTGYSEEQ  400

Qy  565 LPECVKSL  572
Db  401 LMDCARLL  408

Qy  206 ILIDWLIEVHHDKFDLINETLFLTVNLIDRFLSKQNVMRKK-LQLVGLVALLLACKYEEVS 264
Db  448 QPYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTPIFNFLWFYLKAARANPEV 507

Qy  265 VP---VVEDLVLISDKAYTRNDVLEMEKTMLSTLQFNISLPTQYFFLKRFLKAAQADKKC  321
Db  508 ERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISAYQRVIKVHVRRTTDNELPE 567

Qy  322 EVLASFLIELALVEYEMLRFPPSLLAATSVVTAQCTLDGSRKWNSTCEFHCHYSEDQLME  381
Db  382 CSRKL  386

Qy  568 CVKSL  572
```

RESULT 9

```
S65734
mitosis-specific cyclin 1b - Arabidopsis thaliana
N;Alternate names: B-type cyclin; group I cyclin
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 16-Jul-1999
C;Accession: S65734; S45293
R;Day, I.S.; Reddy, A.S.N.; Golovkin, M.
   Plant Mol. Biol. 30, 565-575, 1996
A;Title: Isolation of a new mitotic-like cyclin from Arabidopsis: complementation of...
A;Reference number: S65734; MUID:96189269
A;Accession: S65734
A;Molecule type: mRNA
A;Residues: 1-445 <DAY>
A;Cross-references: EMBL:L27223; NID:g1360645; PIDN:AAB02028.1; PID:g1360646
R;Day, I.S.; Reddy, A.S.N.
   Biochim. Biophys. Acta 1218, 115-118, 1994
A;Title: Cloning of a family of cyclins from Arabidopsis thaliana.
A;Reference number: S45293; MUID:94250688
A;Accession: S45293
A;Molecule type: mRNA
A;Residues: 213-276 <DAW>
A;Cross-references: EMBL:L27223
C;Genetics:
C;Gene: cyclb
C;Superfamily: cyclin
C;Keywords: cell cycle control; cell division control; mitosis
```

Query Match 7.9%; Score 234.5; DB 2; Length 445;
Best Local Similarity 24.9%; Pred. No. 3.2e-07;
Matches 74; Conservative 67; Mismatches 133; Indels 23; Gaps 6;

```
Qy  286 PSIFFDSGGSEFSEKSSSDSP-----ISHSRSLYLQFKEQFCRSTIPNDFGGSCEEIHSEL 341
Db  119 PVEVIETKKEVTKKEVAMSPKNKKVTYSSVLSARSK----------AACGIVNKPKI      165

Qy  342 LRFDEDEVEESYLRLRERERSHAYMRDCAKAYCSRM--DNTGLIPRLRSIMVQWIVKQC   398
Db  166 IDIDESDKDNHLAAVEVVDDMYSFYKEVEKRSQPRMYMHIQTEMNEKMRAILIDWLLEVH  225

Qy  399 SDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEENQPYNSIRKRNF  458
Db  226 IKFELNLETLYLTVNIIDRFLSVKAV-PKRRELQLVCISALLIASKYEEIWP-PQVNDLVY 283

Qy  459 TIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTS  518
Db  284 VTDN-AYSSRQILVMEKAILGNLEWYLTVPFTQYVFLVRFIKASMSDPEMRNVHFLAELG  342

Qy  519 LSDQTQLCFWPSTVAAALVVLACIEHNKISAYQRVIKVHVRRTTDNELPECVKSLDWL    575
Db  343 MMHYDTLTFCPSMQAASAVTTARCSLNKSPAWTDTLQFHTGYTESEIMDCSKLLAFL    399
```

RESULT 10

```
T03675
cyclin 2 - rice
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Accession: T03675
R;Sauter, M.; Mekhedov, S.L.; Kende, H.
   Plant J. 7, 623-632, 1995
A;Title: Gibberellin promotes histone H1 kinase activity and the expression of cdc2 a...
A;Reference number: Z14999; MUID:95261415
A;Accession: T03675
A;Molecule type: mRNA
A;Residues: 1-419 <SAU>
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:X82036; NID:g1694891; PIDN:CAA57556.1; PID:g1694892
A;Experimental source: cv. PingGaew53
C;Genetics:
C;Gene: cyc2
C;Superfamily: cyclin
```

RESULT 11
protein F2D10.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B86339
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C;A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: B86339
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-460 <STO>
A;Cross-references: GB:AE005172; NID:g8886952; PIDN:AAF80638.1; GSPDB:GN00141
A;Genetics:
A;Gene: F2D10.10
A;Map position: 1
C;Superfamily: cyclin

Query Match	7.9%;	Score 233;	DB 2; Length 460;
Best Local Similarity	22.6%;	Pred. No. 4.2e-07;	
Matches 78;	Conservative 77;	Mismatches 138;	Indels 52; Gaps 11;

Qy   250 SEKFSEEVSD-----SLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGGSEFSEKSSSSDSP- 305
           : ||:   :   :||| :||| :::||:: ::|||| :|| |: |||:|:
Db   109 TRKFAAQLADHKPHIRDEETKPDSVSSEEPE---------TIIDVDESDKEGGDSNEPM 160

Qy   306 -ISHSRSLYLQFFKEQFCRSTPNDFGSSCEEIHSELLRFDDEEVESYLRLRERERS-- 362
          :| ||:|||:||| : |||:||:|::::::|:|| ::||| ::| :|
Db   161 FVQHTEAMLEEIEQM---------DADKEEPVIDIDACDKNNP 202

Qy   363 --------HAYMRDCAKAYC-----SRMDN-TGLIPRLRSIMVQWIVKQCSDMGLQQETL 408
                  | : ::: ||:|| :|:|||:||||||||||||||||||||
Db   203 LAAVEYIHDMHTFYKNFEKLSCVPPNYMDNOQDLNERMRGILIDWLIEVHYKFELMEETL 262

Qy   409 FLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEE--NQPYNSIRKRNFTIQNLRYSR 467
          | :::|||:| :|||||||| |||||||||||||||| ||:|| ||||||| ||||:|
Db   263 YLTINVIDRFLAVHQIYRKK-LQLVGVTALLLACKYEEVSVP---VVDDLIISDKAYSR 318

Qy   468 HEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTSLSDQTQLCF 527
          || | ||||| ||||||| || |||||||||||| |||||||||||||||||||||||| |
Db   319 REVLDMEKLMANTLQFNFSLPTPYVFMKRFLKAAQSDKKLEILSFFMIELCLVEYEMLEY 378

Qy   528 WPSTVAAALVVLACIEHNKISAYQRVIKVHVHVRTTDNELPECVKSL 572
          ||| ||||||||||||||| ||||||||||||||||||||||||||
Db   379 LPSKLAASAIYIAQCTLKGFEEMSKTCEFHTGYNEKQLLACARKM 423

RESULT 12
T03021
mitosis-specific cyclin CYM, B-type - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Accession: T03021
R;Ito, M.; Criqui, M.C.; Sakabe, M.; Ohno, T.; Hata, S.; Kouchi, H.; Hashimoto, J.; F
Plant J. 11, 983-992, 1997
A;Title: Cell-cycle regulated transcription of A- and B-type plant cyclin genes in sy
A;Reference number: Z14823; MUID:97336294
A;Accession: T03021
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-446 <ITO>
A;Cross-references: EMBL:D89635; NID:g2196452; PIDN:BAA20425.1; PID:g2196453
C;Note: G2 and M phases of the cell cycle
C;Genetics:
A;Gene: CYM
A;Superfamily: cyclin
C;Keywords: cell cycle control; cell division control; mitosis

Query Match	7.9%;	Score 232.5;	DB 2; Length 446;
Best Local Similarity	20.4%;	Pred. No. 4.3e-07;	
Matches 94;	Conservative 89;	Mismatches 156;	Indels 121; Gaps 15;

Qy   159 SFSRSDVTFAGHVSNSRSLNFESENKESDVVSISGVE----------------YCSK-FGSVT 205
          :| :: |||| | || |: ::|: :|:   :: |||| ||| |
Db   19 ALKOKNMAAAAQGRNRKALGDIGNN-----MVTVRGVEGKPLPQRPITRGFCAQLLANAQ 73

Qy   206 GGADNEEIEISKPSSFVEADSSL----------GSAKE-----LKPELEIVGCVSDLAC 249
          | ::| |: : | : | |||:| |||| |: |: |
Db   74 AAAENQ------KKSMVVNGDAPIVAKGYLPVKGAAKKFEVQKAAAVKRPDVI------- 120

Qy   250 SEKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGGSEFSEKSSSSDSPISHS 309
          ||||||||| :||| : || :| | :: |||| || ||||||||||||| |
Db   121 ------EISPDTEEQVKENKQK---------SQPEITARMAILIDWLIEVHHKFELSQETLYLTINI 248

Qy   310 RSLYLQFFKEQFCRSTPINDFGSSC------EEEIHSELLRFDDEEVESYLR 355
          ||||||:|||||||||:|||||| | :::::||||||||||||| |
Db   146 -----KKATLTSTLTARSKAACGLSHKPKVQIVDIDAADVNNELAVVEVEDIINFYK 198

Qy   356 LRERE-RSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGL 414
           | :| :| | |:||||| |:|||:|:||||||||||||||||||||||||||| ||
Db   199 IAENESRIHDYMD-------------SOPEITARMAILIDWLIEVHHKFELSQETLYLTINI 248

Qy   415 LDRFLSKGSFKSERTLILVGIASLTLATRIEE--NQPYNSIRKRNFTIQNLRYSRHEVVA 472
          :|:|:| :|||||||| |||||||||||||||| ||:|| ||||||| ||||:|||||
Db   249 VDRYLAV-TTTSRRELQLVGMSAMLIASKYEEIWAPEVNDF---VCISDKAYSHEQVLG 303

Qy   473 MEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTV 532
          ||||||||||||| || |||||||||||| |||||||||||||||||||||||| ||||
Db   304 MEKRILGQLEWLITVPTPYVFLRYIKAAVSNAQMENAVYFLAELGLMNYAINIYCPSMI 363

Qy   533 AAALVVLACIEHHKISAYQRVIKVHVRTTDNELPECVKSL 572
          |||||||||||||| ||||||||||||||||||||||||
Db   364 AASAVVYVAQHTLNCTPFWNDTLKLHTGFSESOLLGCAKLL 403

RESULT 13
T10527
cyclin B1d-11 - yellow lupine

C;Species: Lupinus luteus (yellow lupine)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
R;Deckert, J.; Jelenska, J.; Zaborowska, Z.; Legocki, A.B.
Acta Biochim. Pol. 44, 37-42, 1997
A;Title: Isolation and classification of a family of cyclin gene homologues in Lupinus 1
A;Reference number: 217072; MUID:97385338
A;Accession: T10527
A;Molecule type: mRNA
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-452 <DEC>
A;Cross-references: EMBL:044857; NID:g3251102; PIDN:AAC24245.1; PID:g3251103
A;Experimental source: cultivar ventus: clone CycB1d-11
C;Superfamily: cyclin
C;Keywords: cell cycle control; cell division control; mitosis

Query Match   7.8%; Score 229; DB 2; Length 452;
Best Local Similarity   26.9%; Pred. No. 7.3e-07;
Matches   78; Conservative   56; Mismatches 120; Indels 36; Gaps   8;

Qy   293 GSEFSEKSSSDSPISHSRS------LYLQFKEQFCRSTIPNDFGSSCEEIHSELLRFDDE 347
         ::|:||| |:| ||||||||||||||||||||||||||||||
Db   137 GGENKKKSRTLTSVLPARSKAACGLTNKPKEKI----IDIDAGDSGNELAAVEYI----E 188

Qy   348 EVEESYLRLRERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVYKQCSDMGLQOET 407
         |||||:| | :||| ||||||||||||||||||||||||||||:| |:|| || ||
Db   189 DIYKFYKLAENENRPHQYMD-------SQPD----INEKMRAILVDWLINVHVKFDLSLET 238

Qy   408 LFLGVGLLLDRFLSKGSFKSSERTLILVGIASLTLATRIEENQP------YNSIRKRNFT 462
         |||:||||||||||||||||||||||||||||||||||||||| :| ||||| |
Db   239 LYLTINIIDRFLALKTY-PRKELQLVGISAMLMASKYEEIWPPEVDEFVCLSDRAFI--- 294

Qy   463 LRYSRHEVVAMEWLVQEVLNFKCFTPTPIFNFLWFYLKAARANPEVERKAKSLAVTSLSDQ 522
         ||||||||||||||||||||||||||||||||||||||||||||:||| | ||||||||
Db   295 ----HEEVLAMEKIILGKLEWTLTVPPYVFLVRFIKASVPDQOELENMAHFLSELGMMHY 350

Qy   523 TQLCFWPSTVAAALVVLACIEHNKISAYQRVIKVHVHVRTTDNELPECVKSL 572
         |: | ||| | | :|||| | |||| || |:::   :| ::| |||
Db   351 GTLMVCPSMIAASAVFAARCILNKTPIWNEYLKLHTGYSKEQLMDCAKLL 400

RESULT 14
S16521
mitosis-specific cyclin C13-1 - carrot (fragment)
N;Alternate names: A-type cyclin
C;Species: Daucus carota (carrot)
C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 16-Jul-1999
R;Hata, S.; Kouchi, H.; Suzuka, I.; Ishii, T.
EMBO J. 10, 2681-2688, 1991
A;Title: Isolation and characterization of cDNA clones for plant cyclins.
A;Reference number: S16521; MUID:91330894
A;Accession: S16521
A;Molecule type: mRNA
A;Residues: 1-341 <HAT>
A;Cross-references: EMBL:X62819; NID:g18359; PIDN:CAA44631.1; PID:g829260
C;Superfamily: cyclin
C;Keywords: cell cycle control; cell division control; mitosis

Query Match   7.7%; Score 227.5; DB 2; Length 341;
Best Local Similarity   27.7%; Pred. No. 6.2e-07;
Matches   89; Conservative   51; Mismatches 106; Indels 75; Gaps 14;

Qy   298 EKSSSDSPISHSRSLYL-QFKEQFC--------RSTIPNDFGSSCEEIHSELLRFDD 346
         |:::|| || ||| | | :||| ||||||||||||||||||||||||
Db   19 EISNSSAVSGNEDLLCREFVPKVCVAQKKRKRGVKEDVGVDFGE----------KFDD 67

Qy   347 EEVEES-------YLRLRERERSHA----YMRDCAKAYCSRMDNTGLIPRLRSIMVQWIV 395
         :::::| |||||:||||| ||||||||||||||||||||||||||||||
Db   68 PQMCSAYSDVYEYLKQMEMETKRRPMMNYIEQVQKDVTSNM-------RGVLVDWLIV 118

RESULT 15
A96803
probable mitotic cyclin a2-type [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: A96803
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: A96803
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <STO>
A;Cross-references: GB:AE005173; NID:g11079479; PIDN:AAG29191.1; GSPDB:GN00141
A;Genetics:
A;Gene: F2P24.10
A;Map position: 1
C;Superfamily: cyclin

Query Match   7.7%; Score 227.5; DB 2; Length 454;
Best Local Similarity   24.8%; Pred. No. 9.1e-07;
Matches 105; Conservative   76; Mismatches 195; Indels 47; Gaps 14;

Qy   172 SNRSLNFESENKESDVVSVTSGVEVCSKFGSVTGGADNEIEISKP---SSFVEADSSL 228
         :|||||:||:|:::| | ||:| ||| | | | || || | :||:| :||
Db   3 SSSRNLSQENPIPRPNLAKTRTSLRDVGNRRAPLGDITNQKNGSRNPSPSSTLVNCSNKI 62

Qy   229 GSAKEL-KPELEIVGCVSDLACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYTPS 287
         |||:| | |::| ||:| :|:||:||||||||||| | ||:: | |:||| |
Db   63 GQSKRAPKP---------ALSRNWNLGILDSGLPPKPNAKSNIIVPYEDTELLQSSDS 111

Qy   288 IFFDSG--SEFSEKSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSCEEIHSELLRFD 345
         | ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   112 LLCSSPALSLDASPYQSDPSISTHDSLTNHVVDYMVEST---TDDGNDDDDD----EIVNID 166

Qy   346 DEEVE---------ESYLRLRERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVIK 396
         ::::| :|||||:||||| |||||||||||||||||||||||||||| |
Db   167 SDLMDPQLCASFACDIYEHLRVSEVNKRPALD----YMERTQSS-INASMSILIDWLVE 221

Qy   397 QCSDMGLQQETLFLGVGLLDRFLSKGSFKSSERTLILVGIASLTLATRIEENQPYNSIRKR 456
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db   222 VAEEYRLSPETLYLAVNVDRYLT-GNAIKQNLQLLGVTCMMIAAKYEE---VCVPQVE 277

Qy   457 NFT-IQNLRYSRHEVVAMEWLVQEVLNFKCFTPTPIFNFLWFYLKAARANPEV 510
         ||| ||||||||||||||||||||||||||||||||||||||||||||| :|
Db   278 DFCYITDNYLRNELLEMESSVLNYLKFELTTPFAKCFLRRFLRAAQGRKEVPSLLSECL 337

Qy   396 KQCSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEENQPYNSIRK 455
         |||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db   119 EVSLEYKLLPETLYLAISYVDKRYLSVNVLNRQK-LQLLGVSSPLIASKYEEIRPKN--V 174

Qy   456 RNFT-IQNLRYSRHEVVAMEWLVQEVLNFKCFTPTPIFNFLWFYLKAARANPEV----ER 509
         |||| ||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   175 ADFVDITDNTYSQQEVVKMEADLIKTLKFEMGSPTVKTFLGF-IRAVQENPDVPKLRFEF 233

Qy   510 KAKSLAVTSLSDQTOLCFWPSTVAAALVVLA-----------CIEHNKISAYQRVIKVHV 558
         |||||||||||||| | || | | | | |:||| ||| |||| |
Db   234 LANYLAELSLILDYGCLEFVPSLIAASVTFLARFTIRPNVNPWSIALQKCSGYK----- 286

Qy   559 RTTTDNELPECVKSL-DWLLGQ 578
         ::|| || || || || |||
Db   287 ---SKDLKECVLLHDLQMGR 304

```
Qy  511 AKSLAVTSLSDQTQLCFWPSTVAAALVVLACIE-HNKISAYQRVIKVHVRTTDNELPECV 569
            |  | |   ||: || |||: | ||       :  :   ||    ||
Db  338 ACYLTELSLLDYAMLRYAPSLVAASAVFLAQYTLHPSRKPWNATLEHYTSYRAKHMEACV 397

Qy  570 KSL 572
            |:|
Db  398 KNL 400
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Search completed: July 23, 2002, 14:22:49
Job time: 233 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2002, 14:18:35 ; Search time 14.67 Seconds
                                         (without alignments)
                                         962.372 Million cell updates/sec

Title: US-09-821-839-2
Perfect score: 2952
Sequence: 1 MKEIAMRNSKRKPEPTPFAG.........RTTDNELPECVKSLDWLLGQ 578

Scoring table: BLOSUM62
Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
   1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
   2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
   3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
   4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
   5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
   6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	201.5	6.8	432	1	US-08-522-166-8	Sequence 8, Appli
2	201.5	6.8	432	1	US-08-488-382A-8	Sequence 8, Appli
3	201.5	6.8	432	2	US-08-480-912-8	Sequence 8, Appli
4	194	6.6	433	3	US-08-522-166-7	Sequence 7, Appli
5	194	6.6	433	1	US-08-488-382A-7	Sequence 7, Appli
6	194	6.6	433	2	US-08-480-912-7	Sequence 7, Appli
7	188.5	6.4	150	2	US-08-460-694-3	Sequence 3, Appli
8	188.5	6.4	150	3	US-08-460-744-3	Sequence 3, Appli
9	188.5	6.4	150	4	US-09-092-770-3	Sequence 3, Appli
10	184.5	6.2	404	2	US-09-222-851-3	Sequence 3, Appli
11	184.5	6.2	404	2	US-08-460-744-5	Sequence 5, Appli
12	184	6.2	149	3	US-07-667-711B-5	Sequence 5, Appli
13	184	6.2	149	4	US-08-460-744-5	Sequence 5, Appli
14	184	6.2	149	3	US-09-092-770-4	Sequence 4, Appli
15	183	6.2	173	4	US-07-667-711B-5	Sequence 5, Appli
16	179.5	6.1	403	2	US-09-092-770-4	Sequence 4, Appli
17	179.5	6.1	403	4	US-09-222-851-4	Sequence 4, Appli
18	168	5.7	492	1	US-08-463-090B-10	Sequence 10, Appli
19	163.5	5.5	148	2	US-08-460-694-6	Sequence 6, Appli
20	163.5	5.5	148	3	US-07-667-711B-6	Sequence 6, Appli
21	163.5	5.5	148	3	US-08-460-744-6	Sequence 6, Appli
22	160	5.4	171	1	US-08-193-977-5	Sequence 5, Appli
23	156.5	5.3	106	1	US-08-464-517-25	Sequence 25, Appli
24	156.5	5.3	106	2	US-08-246-361A-25	Sequence 25, Appli
25	156.5	5.3	106	3	US-08-463-772-25	Sequence 25, Appli
26	156.5	5.3	106	5	PCT-US93-05000-25	Sequence 25, Appli
27	156.5	5.3	295	2	US-08-464-517-20	Sequence 20, Appli
28	156.5	5.3	295	2	US-08-246-361A-20	Sequence 20, Appli
29	156.5	5.3	295	3	US-08-463-772-20	Sequence 20, Appli
30	156.5	5.3	295	5	PCT-US93-05000-20	Sequence 20, Appli
31	155.5	5.3	295	1	US-07-947-120-8	Sequence 8, Appli
32	155.5	5.3	295	2	US-08-472-893A-8	Sequence 8, Appli
33	155.5	5.3	295	2	US-08-460-694-2	Sequence 2, Appli
34	155.5	5.3	150	3	US-08-460-744-2	Sequence 2, Appli
35	155.5	5.3	295	3	US-07-667-711B-2	Sequence 2, Appli
36	155.5	5.3	295	3	US-08-947-492-8	Sequence 8, Appli
37	155.5	5.3	618	2	US-08-770-761A-8	Sequence 8, Appli
38	155.5	5.3	647	2	US-08-770-761A-3	Sequence 3, Appli
39	155.5	5.3	660	2	US-08-770-761A-2	Sequence 2, Appli
40	155.5	5.3	662	2	US-08-770-761A-2	Sequence 2, Appli
41	155.5	5.2	705	2	US-08-770-761A-7	Sequence 7, Appli
42	153.5	5.2	295	2	US-08-464-517-19	Sequence 19, Appli
43	153.5	5.2	295	2	US-08-246-361A-19	Sequence 19, Appli
44	153.5	5.2	295	3	US-08-463-772-19	Sequence 19, Appli
45	153.5	5.2	295	5	PCT-US93-05000-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-522-166-8
Sequence 8, Application US/08522166
Patent No. 5783661

GENERAL INFORMATION:
 APPLICANT: Roberts, J.M.;Ohtsubo, M; Koff, A.C.; Cross, F.
 TITLE OF INVENTION: Human Cyclin E
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
  ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
  STREET: 2800 Pacific First Center, 1420 Fifth Avenue
  CITY: Seattle
  STATE: Washington
  COUNTRY: USA
  ZIP: 98101-2347
 COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
  COMPUTER: IBM PC Compatible/Pentium
  OPERATING SYSTEM: MS-Windows 3.1
  SOFTWARE: Word for Windows-6.0
 CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/522,166
  FILING DATE: June 7, 1995
  CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 07/764,309
  FILING DATE: September 20, 1991
 ATTORNEY/AGENT INFORMATION:
  NAME: Sheiness, Diana K.
  REGISTRATION NUMBER: 35,356
  REFERENCE/DOCKET NUMBER: EHRO-1-8597
 TELECOMMUNICATION INFORMATION:
  TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
  TELEFAX: 1-206-224-0779
 INFORMATION FOR SEQ ID NO: 8:
  SEQUENCE CHARACTERISTICS:
   LENGTH: 432 amino acids
   TYPE: amino acid
   STRANDEDNESS: single
   TOPOLOGY: linear
  MOLECULE TYPE: protein
  DESCRIPTION: Cyclin B polypeptide sequence; Figure 3
  ORIGINAL SOURCE:
   ORGANISM: Homo Sapiens

US-08-522-166-8

Query Match   6.8%;   Score 201.5; DB 1; Length 432;
Best Local Similarity   24.1%; Pred. No. 7.8e-10;
Matches   90; Conservative   67; Mismatches 136; Indels   81; Gaps   13;

RESULT 2
US-08-488-382A-8
Sequence 8, Application US/08488382A
Patent No. 5807698
GENERAL INFORMATION:
  APPLICANT: Roberts, J.M.;Ohtsubo, M; Koff, A.C.; Cross, F.
  TITLE OF INVENTION: Human Cyclin E
  NUMBER OF SEQUENCES: 8
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
    STREET: 2800 Pacific First Center, 1420 Fifth Avenue
    CITY: Seattle
    STATE: Washington
    COUNTRY: USA
    ZIP: 98101-2347
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
    COMPUTER: IBM PC Compatible/Pentium
    OPERATING SYSTEM: MS-Windows 3.1
    SOFTWARE: Word for Windows-6.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/488,382A
    FILING DATE: June 7, 1995
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 07/764,309
    FILING DATE: September 20, 1991
  ATTORNEY/AGENT INFORMATION:
    NAME: Sheiness, Diana K.
    REGISTRATION NUMBER: 35,356
    REFERENCE/DOCKET NUMBER: FHRO-1-8600
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
    TELEFAX: 1-206-224-0779
INFORMATION FOR SEQ ID NO: 8:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 432 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  DESCRIPTION: Cyclin B polypeptide sequence; Figure 3
  ORIGINAL SOURCE:

Qy   209 DNEEIEISKPS---------------SFVEADSSLGSAKELKPELEIVGCVVSDIACSEKF---- 253
           ||||||||||| ||:| |:|| | ||| ||||||:|||||| |
Db   29   DQENINPEKAAPVQQPRTRAALAVLKSGNPRGLAQQORPKTRRVAPLKDLPVNDEHVTVP   88

Qy   254 ------SEEVSDSLD-DESSEQRSEIIYSQYSDFDYSDYTPSIFFDSG---------------SE 295
                 :||| | ||| :| | |: : ||
Db   89   PWKANSKQPAFTIHVDEAEKEAQKKPAESQKIERED---ALAAFNSAISLPGPRKPLVPLD   145

Qy   296 FSEKSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSCEEIIHSELLRFDDEEVEESYLR   355
           |:| | ||| : |||: | : | | : :|| :|||||||||
Db   146 YPMDGSFESPHTMDMSIVLEDEKPVSVNENPD------------------YHEDIH----   187

Qy   356 LRERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLL   415
           || :|| |:| : | || |: |||||:|||||||:| : | :|||:|| | |||:
Db   188 EMEVK-------CKPKVGYMKKQPDITNSMRAILVDWLVEVGEEYKLQNETLHLAVNYI   239

Qy   416 DRFLSKGFKSERTLILVGIASLTLATRIEENQP----------YNSIRKRNFTIQNLRYSRH   468
           ||||| ||||||| ||| : :|| | | :| |||||| :|||
Db   240 DRFLSSMSVLRGK-LQLVGTAAMLLASKFEEIYPPEVAEFVV---------ITDDTYTKK   289

Qy   469 EVVAMEWLVQEVLNFKCFTPTIFNFL-WFYLKAARANPEVERKAKSLAVTSLSD-QTQLC   526
           :: || | ||||||| |: ||| | ||||||| |||| |||||| | | :||:|
Db   290 QVLRMEHLVLKVLTFDLAAPTVNQFLTQYFLHQOPANCKVESLAMFLGELSLIDADPYLK   349

Qy   527 FWPSTVAAALVVLA   540
           | |:| | ||
Db   350 YLPSVIAGAAFHLA   363

ORGANISM: Homo Sapiens
US-08-488-382A-8

Best Local Similarity   6.8%;
Matches 90;   Conservative 67;   Mismatches 136;   Indels 81;   Gaps 13;
Query Match   24.1%;   Score 201.5;   DB 1;   Length 432;   Pred. No. 7.8e-10;

Qy   209 DNEEIEISKPS----------------SFVEADSSLGSAKELKPELEIVGCVVSDIACSEKF---- 253
           ||||||||||| ||:| |:|| | ||| ||||||:|||||| |
Db   29   DQENINPEKAAPVQQPRTRAALAVLKSGNPRGLAQQORPKTRRVAPLKDLPVNDEHVTVP   88

Qy   254 -------SEEVSDSLD-DESSEQRSEIIYSQYSDFDYSDYTPSIFFDSG--------------SE 295
                  :||| | ||| :| | |: : ||
Db   89   PWKANSKQPAFTIHVDEAEKEAQKKPAESQKIERED---ALAAFNSAISLPGPRKPLVPLD   145

Qy   296 FSEKSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSCEEIIHSELLRFDDEEVEESYLR   355
           |:| | ||| : |||: | : | | : :|| :|||||||||
Db   146 YPMDGSFESPHTMDMSIVLEDEKPVSVNENPD------------------YHEDIH----   187

Qy   356 LRERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLL   415
           || :|| |:| : | || |: |||||:|||||||:| : | :|||:|| | |||:
Db   188 EMEVK-------CKPKVGYMKKQPDITNSMRAILVDWLVEVGEEYKLQNETLHLAVNYI   239

Qy   416 DRFLSKGFKSERTLILVGIASLTLATRIEENQP----------YNSIRKRNFTIQNLRYSRH   468
           ||||| ||||||| ||| : :|| | | :| |||||| :|||
Db   240 DRFLSSMSVLRGK-LQLVGTAAMLLASKFEEIYPPEVAEFVV---------ITDDTYTKK   289

Qy   469 EVVAMEWLVQEVLNFKCFTPTIFNFL-WFYLKAARANPEVERKAKSLAVTSLSD-QTQLC   526
           :: || | ||||||| |: ||| | ||||||| |||| |||||| | | :||:|
Db   290 QVLRMEHLVLKVLTFDLAAPTVNQFLTQYFLHQOPANCKVESLAMFLGELSLIDADPYLK   349

Qy   527 FWPSTVAAALVVLA   540
           | |:| | ||
Db   350 YLPSVIAGAAFHLA   363

RESULT 3
US-08-480-912-8
Sequence 8, Application US/08480912
Patent No. 5861259
GENERAL INFORMATION:
  APPLICANT: Roberts, J.M.;Ohtsubo, M; Koff, A.C.; Cross, F.
  TITLE OF INVENTION: Immunoassays for Detection of Human Cyclin E
  NUMBER OF SEQUENCES: 8
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
    STREET: 2800 Pacific First Center, 1420 Fifth Avenue
    CITY: Seattle
    STATE: Washington
    COUNTRY: USA
    ZIP: 98101-2347
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
    COMPUTER: IBM PC Compatible/Pentium
    OPERATING SYSTEM: MS-Windows 3.1
    SOFTWARE: Word for Windows-6.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/480,912
    FILING DATE: June 7, 1995
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 07/764,309
    FILING DATE: September 20, 1991
  ATTORNEY/AGENT INFORMATION:
    NAME: Sheiness, Diana K.
    REGISTRATION NUMBER: 35,356
    REFERENCE/DOCKET NUMBER: FHRO-1-8599
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
    TELEFAX: 1-206-224-0779
INFORMATION FOR SEQ ID NO: 8:
  SEQUENCE CHARACTERISTICS:

```
;  LENGTH: 432 amino acids
;  TYPE: amino acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
;  DESCRIPTION: Cyclin B polypeptide sequence; Figure 3
;  ORIGINAL SOURCE:
;  ORGANISM: Homo sapiens
US-08-480-912-8

Query Match    6.8%; Score 201.5; DB 2; Length 432;
Best Local Similarity    24.1%; Pred. No. 7.8e-10;
Matches  90; Conservative  67; Mismatches 136; Indels  81; Gaps  13;

Qy    209 DNEEIEISKPS------------------SFVEADSSLGSAKELKPELEIVGCCVSDLACSEKF----- 253
              : | | :| |:                    |:| :| :| || ||:  |:|:|
Db     29 DQENINPEKAAPVQQPRTRAALAVLKSGNPRGLAQOOORPKTRRVAPLKDLPVNDEHVTVP        88

Qy    254 -----SEEYSDSLD-DESSEQRSEIYSQYSDFDYSDYTPSIFFDSG----------------SE     295
                :|: :|:|:   ||::| : ||::| : || ::|| :::|  ||| |:
Db     89 PWKANSKQPAFTIHVDEAEKEAQKKPAESQKIERED---ALAFNSAISLPGPRKPLVPLD         145

Qy    296 FSEKSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSSCEEEIHSELLRFDDEEVEESYLR      355
              :|:: : |: :|  ::|  | :    |  |: | ::||||:|  |: ::||:
Db    146 YPMDGSFESPHTMDMSIVLEDEKPVSVNENPD-----YHEDIH---------------TYLR      187

Qy    356 LRERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLL      415
              |: | |:|:| ||: :| :|:| | || | :|:|| | :: |:| |: | |::||:||
Db    188 EMEVK----------CKPKVGYMKKQPDITNSMRAILVDWLVEVGEEYKLQNETLHLAVNYI      239

Qy    416 DRFLSKGSPFKSERTLILVGIASILTLATRIEENQP-------YNSIRKRNFTIQNLRYSRH      468
              ||||| |  |:|| |::| || : |:|: :|  |       |:|:|||||: ::|:|||
Db    240 DRFLSSMSVLRGK-LQLVGTAAMLLASKFEEIYPPEVAEFVY----------ITDDTYTKK      289

Qy    469 EVVAMEWLVQEVLNFKCFPTPIFNFL-WFYLKAARANPEVERKAKSLAVTSLSD-QTQLC      526
              ::| ||:|| ||| : |||| |  |: | || | ||| :  |::|||:|:: :| | :||
Db    290 QVLRMEHLVLKVLFDLLAAPTVNQFLTQYFLHQQPANCKVESLAMPLIGELSLIIDADPYLK      349

Qy    527 FWPSTVAAALVVLA       540
              || : | ||| | |
Db    350 YLPSVIAGAAFHLA       363
```

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;  REGISTRATION NUMBER: 35,356
;  REFERENCE/DOCKET NUMBER: FHRO-1-8597
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 1-206-682-8100; 1-206-224-8597
;  TELEFAX: 1-206-224-0779; 1-206-224-0735 (direct)
;  INFORMATION FOR SEQ ID NO: 7:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 433 amino acids
;  TYPE: amino acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
;  DESCRIPTION: Cyclin A polypeptide sequence; Figure 3
;  ORIGINAL SOURCE:
;  ORGANISM: Homo sapiens
US-08-522-166-7

Query Match    6.8%; Score 194; DB 1; Length 433;
Best Local Similarity    22.2%; Pred. No. 3.7e-09;
Matches  87; Conservative  64; Mismatches 169; Indels  72; Gaps  14;

Qy    170 HVSNSRSLNFESENKESDVVSVIS--GVEYCSKFGSVTGGADNEIEISKPSSFVEADSS      227
              |:|:|||||| |:||:|:|||:|:   |::|:|| :|| :| :|:  |::| :|| ||
Db     12 NAENKAKINMAGARKVPTAPAATSKPGLRPRTALGDI-GNKVSEQLQAKMPMKKEAKPSA       70

Qy    228 LGSA--KELKPELEIVGCVSDLACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYT      285
              ||:|   |:|| |:|:|  ::: : : | :|| |:  |::||:|| : ||:||:|:|:||
Db     71 TGKVIDKLPKPLEKVPMLVPPVYSEPVPEPEPEPEPEPVKEEK---------------LS      116

Qy    286 PS-IFFDSGSEFSEKSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSSCEEEIHSELLRF      344
              || |||| | |::||:|:||||:|||:|| |:|::|| || :||:|:  ||||:| |
Db    117 PEPILVDIASPSPMETSGCAPA-----------------EEQLCQA-----FSDVILAV      153

Qy    345 DDEEVEE--------------SYLRIRERERSHAYMRDCAKAYCSRMDNTGLIPRLRSI      389
              :: :|:|               |:|: | | |:||:|| : :|| | |:: | || |
Db    154 NDVDAEDGADPNLCSEYBKDIYAYLRQLEEEQA------VRPKYLLBREVTG---NMRAI      204

Qy    390 MVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGS-FKSERTLILVGIASILTLATRIEENQ      448
              ||||:| |:|| |:||| | |:||||||:||||  ||| |:|::||| :: || :||:| |
Db    205 LIDWLVQVQMKFRLLQETMYMTVSIIDRFMQNNCVFK----KMIQLVGVTAMFIASKYEEFY      262

Qy    449 PYNSIRKRNFTIQNLRYSRHEVAVAMEWLVQEVLNFKCFPTPIFNFLWFYLKAARANPEVE      508
              | |:|||||:||| ||:|: |:| |||||:|||||:| ||||:|||| |||| |: | :|
Db    263 P-PEIGDFAFVTDN-TYTKHQIRQMEMKILRALNEFGLGRPLHFLRRASKIGEVKVEQH      320

Qy    509 RKAKSLAVTSLSDQTQLCFWPSTVAAALVVLA      540
              | : ||||:|:| ||:| | || | ||| | |
Db    321 TLAKYIMELITMLDYDMVHFPPSQIAAGAFCLA      352
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RESULT    4
US-08-522-166-7
;  Sequence 7, Application US/08522166
;  Patent No. 5783661
;  GENERAL INFORMATION:
;  APPLICANT: Roberts, J.M.;Ohtsubo, M; Koff, A.C.; Cross, F.
;  TITLE OF INVENTION:    Human Cyclin E
;  NUMBER OF SEQUENCES:  8
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
;  STREET: 2800 Pacific First Center, 1420 Fifth Avenue
;  CITY: Seattle
;  STATE: Washington
;  COUNTRY: USA
;  ZIP: 98101-2347
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
;  COMPUTER: IBM Pc Compatible/Pentium
;  OPERATING SYSTEM: MS-Windows 3.1
;  SOFTWARE: Word for Windows 6.0
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/522,166
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```
RESULT    5
US-08-488-382A-7
;  Sequence 7, Application US/08488382A
;  Patent No. 5807698
;  GENERAL INFORMATION:
;  APPLICANT: Roberts, J.M.;Ohtsubo, M; Koff, A.C.; Cross, F.
;  TITLE OF INVENTION:    Human Cyclin E
;  NUMBER OF SEQUENCES:  8
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
;  STREET: 2800 Pacific First Center, 1420 Fifth Avenue
;  CITY: Seattle
;  STATE: Washington
;  COUNTRY: USA
;  ZIP: 98101-2347
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
;  COMPUTER: IBM Pc Compatible/Pentium
;  OPERATING SYSTEM: MS-Windows 3.1
;  SOFTWARE: Word for Windows 6.0
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/488,382A
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;  FILING DATE: June 7, 1995
;  PRIOR APPLICATION DATA:
;  CLASSIFICATION: 530
;  APPLICATION NUMBER: 07/764,309
;  FILING DATE: September 20, 1991
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Sheiness, Diana K.
```

FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 07/764,309
  FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
  NAME: Sheiness, Diana K.
  REGISTRATION NUMBER: 35,356
  REFERENCE/DOCKET NUMBER: FHRO-1-8600
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
  TELEFAX: 1-206-224-0779
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
  LENGTH: 433 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Cyclin A polypeptide sequence; Figure 3
ORIGINAL SOURCE:
  ORGANISM: Homo Sapiens
US-08-488-382A-7

Query Match   6.6%; Score 194; DB 1; Length 433;
Best Local Similarity 22.2%; Pred. No. 3.7e-09;
Matches 87; Conservative 64; Mismatches 169; Indels 72; Gaps 14;

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Qy  170  HVSNSRSLNFESENKESDVVSVIS--GVEYCSKFGSVTGGADNEEIEISKPSSFVEADSS  227
              :|                  |:                 :|| | |
Db   12  NAENKAKINMAGAKRVPTAPAATSKPGLRPRTALGDI-GNKVSEQLQAKMPMKKEAKPSA  70

Qy  228  LGSA--KELKPELEIVGCVSDLACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYT  285
              ||    |||  |  |      |:|||:|  |::|::  |  |:||
Db   71  TGKVIDKKLPKPLEKVPMLVPVPVSEPVPEPEPEPEPEPVKEEK-------------LS  116

Qy  286  PS-IFFDSGSEFSEKSSSDSSPISHSRSLIYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRF  344
             :|:|    |      || | || | |  |      | |  | | :|| |::
Db  117  PEPILVDTASPSPMETSGCAPA----------------EEQLCQA-----  153

Qy  345  DDEEVEE-----------SYLRLRERSHAYMRDCAKAYCSRMDNTGLIPRLRSI  389
           :|:|:              || |   ||    | |:  | || | |:|
Db  154  NDVDAEDGADPNLCSEYBKDIYALRQLEEEQA-----VRPKYLLBREVTG--NMRAI  204

Qy  390  MVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGS-FKSERTLILVGIASLTLATRIEENQ  448
                |:|  | |  | |   ||   | ||        |||   | | |:||  |||
Db  205  LIDWLVQVQMKFRLLQETMYMTVSIIDRFMQNNCVFK--KMLQLVGVTAMFIASKYEEFY  262

Qy  449  PYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVE  508
              |:||  ||  | |||  |:| || |||   | |     |   ||| | | | ||
Db  263  P-PEIGDFAFVTDN-TYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRASKIGEVKVEQH  320

Qy  509  RKAKSLAVTSLSDQTQLCFWPSTVAAALVVLA  540
           |  |  ||    |  ||||  | ||
Db  321  TLAKYLMELTMLDYDMVHFPPSQIAAGAFCLA  352
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RESULT 6
US-08-480-912-7
Sequence 7, Application US/08480912
Patent No. 5861259
GENERAL INFORMATION:
APPLICANT:
  Roberts, J.M.;Ohtsubo, M; Koff, A.C.; Cross, F.
TITLE OF INVENTION: Immunoassays for Detection of Human Cyclin E
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
  STREET: 2800 Pacific First Center, 1420 Fifth Avenue
  CITY: Seattle
  STATE: Washington
  COUNTRY: USA
  ZIP: 98101-2347

COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
  COMPUTER: IBM PC Compatible/Pentium
  OPERATING SYSTEM: MS-Windows 3.1
  SOFTWARE: Word for Windows-6.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/480,912
  FILING DATE: June 7, 1995
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 07/764,309
  FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
  NAME: Sheiness, Diana K.
  REGISTRATION NUMBER: 35,356
  REFERENCE/DOCKET NUMBER: FHRO-1-8599
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
  TELEFAX: 1-206-224-0779
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
  LENGTH: 433 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Cyclin A polypeptide sequence; Figure 3
ORIGINAL SOURCE:
  ORGANISM: Homo Sapiens
US-08-480-912-7

Query Match   6.6%; Score 194; DB 2; Length 433;
Best Local Similarity 22.2%; Pred. No. 3.7e-09;
Matches 87; Conservative 64; Mismatches 169; Indels 72; Gaps 14;

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Qy  170  HVSNSRSLNFESENKESDVVSVIS--GVEYCSKFGSVTGGADNEEIEISKPSSFVEADSS  227
              :|                  |:                 :|| | |
Db   12  NAENKAKINMAGAKRVPTAPAATSKPGLRPRTALGDI-GNKVSEQLQAKMPMKKEAKPSA  70

Qy  228  LGSA--KELKPELEIVGCVSDLACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYT  285
              ||    |||  |  |      |:|||:|  |::|::  |  |:||
Db   71  TGKVIDKKLPKPLEKVPMLVPVPVSEPVPEPEPEPEPEPVKEEK-------------LS  116

Qy  286  PS-IFFDSGSEFSEKSSSDSSPISHSRSLIYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRF  344
             :|:|    |      || | || | |  |      | |  | | :|| |::
Db  117  PEPILVDTASPSPMETSGCAPA----------------EEQLCQA-----  153

Qy  345  DDEEVEE-----------SYLRLRERSHAYMRDCAKAYCSRMDNTGLIPRLRSI  389
           :|:|:              || |   ||    | |:  | || | |:|
Db  154  NDVDAEDGADPNLCSEYBKDIYALRQLEEEQA-----VRPKYLLBREVTG--NMRAI  204

Qy  390  MVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGS-FKSERTLILVGIASLTLATRIEENQ  448
                |:|  | |  | |   ||   | ||        |||   | | |:||  |||
Db  205  LIDWLVQVQMKFRLLQETMYMTVSIIDRFMQNNCVFK--KMLQLVGVTAMFIASKYEEFY  262

Qy  449  PYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVE  508
              |:||  ||  | |||  |:| || |||   | |     |   ||| | | | ||
Db  263  P-PEIGDFAFVTDN-TYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRASKIGEVKVEQH  320

Qy  509  RKAKSLAVTSLSDQTQLCFWPSTVAAALVVLA  540
           |  |  ||    |  ||||  | ||
Db  321  TLAKYLMELTMLDYDMVHFPPSQIAAGAFCLA  352
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RESULT 7
US-08-460-694-3
Sequence 3, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
  STREET: 1100 New York Avenue, N.W., Suite 600
  CITY: Washington
  STATE: DC
  COUNTRY: USA
  ZIP: 20005
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/460,694
  FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
  NAME: McConathy, Evelyn H.
  REGISTRATION NUMBER: 35,279
  REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-371-2600
  TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 150 amino acids
  TYPE: amino acid
  STRANDEDNESS: not relevant
  TOPOLOGY: linear
  MOLECULE TYPE: peptide
US-08-460-694-3

Query Match
Best Local Similarity 36.5%;   Score 188.5;   DB 2;   Length 150;
Matches 58;   Conservative 24;   Mismatches 58;   Pred. No. 2.2e-09;   Indels 19;   Gaps 5;

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Qy 386 LRSIMVQWIVKQCSDMGLQQEFLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIE 445
           :|::|:| |:|: | ||||||:: |||||||| |::||||:||:||:||
Db 1   MRAILVDWLVEVGEEYKLQNETLHLAVNYIDRFLSSMSVLRGK-LQLVGTAAMLLASKFE 59

Qy 446 ENQP-------YNSIRKRNFTIONLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFL-WFY 497
           :|:|:|:|::|:|:|:|| |:|:||:||||| |::| |||:|::|||:|| | ::
Db 60  EIYPPEVAEFVY--------ITDDTYTKKQVLRMEHLVLKVLTFDLAAPTVNQFLTQYF 110

Qy 498 LKAARANPEVERKAKSLAVTSLSD-QTQLCFWPSTVAAA 535
           ||:|:||:|:||:|| ||:|| ::
Db 111 LHQQPANCKVESLAMFLGELSLIDADPYLKILPSVIAGA 149
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RESULT 8
US-08-460-744-3
Sequence 3, Application US/08460744
Patent No. 6107541
GENERAL INFORMATION:
  APPLICANT: Arnold, Andrew
  TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
  NUMBER OF SEQUENCES: 8
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
  STREET: 1100 New York Avenue, N.W., Suite 600
  CITY: Washington
  STATE: DC
  COUNTRY: USA
  ZIP: 20005
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/460,744
  FILING DATE: 02-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
  NAME: McConathy, Evelyn H.
  REGISTRATION NUMBER: 35,279
  REFERENCE/DOCKET NUMBER: 0609.4070005
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-371-2600
  TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 150 amino acids
  TYPE: amino acid
  STRANDEDNESS: not relevant
  TOPOLOGY: linear
  MOLECULE TYPE: peptide
US-08-460-744-3

Query Match
Best Local Similarity 36.5%;   Score 188.5;   DB 3;   Length 150;
Matches 58;   Conservative 24;   Mismatches 58;   Pred. No. 2.2e-09;   Indels 19;   Gaps 5;

```
Qy 386 LRSIMVQWIVKQCSDMGLQQEFLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIE 445
           :|::|:| |:|: | ||||||:: |||||||| |::||||:||:||:||
Db 1   MRAILVDWLVEVGEEYKLQNETLHLAVNYIDRFLSSMSVLRGK-LQLVGTAAMLLASKFE 59

Qy 446 ENQP-------YNSIRKRNFTIONLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFL-WFY 497
           :|:|:|:|::|:|:|:|| |:|:||:||||| |::| |||:|::|||:|| | ::
Db 60  EIYPPEVAEFVY--------ITDDTYTKKQVLRMEHLVLKVLTFDLAAPTVNQFLTQYF 110

Qy 498 LKAARANPEVERKAKSLAVTSLSD-QTQLCFWPSTVAAA 535
           ||:|:||:|:||:|| ||:|| ::
Db 111 LHQQPANCKVESLAMFLGELSLIDADPYLKILPSVIAGA 149
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RESULT 9
US-07-667-711B-3
Sequence 3, Application US/07667711B
Patent No. 6110700
GENERAL INFORMATION:
  APPLICANT: ARNOLD, ANDREW
  TITLE OF INVENTION: Prad1 Cyclin and its cDNA
  NUMBER OF SEQUENCES: 8
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
  STREET: 1100 NEW YORK AVE., NW, SUITE 600
  CITY: WASHINGTON
  STATE: DC
  COUNTRY: USA
  ZIP: 20005
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/667,711B
  FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
  NAME: MCPHAIL, DONALD R.
  REGISTRATION NUMBER: 35,811
  REFERENCE/DOCKET NUMBER: 0609.4070000
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202) 371-2600
  TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 150 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: not relevant
  MOLECULE TYPE: peptide

US-07-667-711B-3

```
Qy   Query Match           6.4%;     Score 188.5;   DB 3;    Length 150;
;    Best Local Similarity 36.5%;    Pred. No. 2.2e-09;
;    Matches  58;  Conservative  24;  Mismatches  58;  Indels  19;  Gaps  5;
;
Qy   386 LRSIMVQWIVKQCSDMGLQQOETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIE 445
         ::| ||||| ::| | ||||  |||| | || |||||| |||||||||| ||||||
Db   1 MRAILVDWLVEVGEYKLQNETLHLAVNYIDRFLSSMSVLRGK-LQLVGTAAMLLASKFE  59

Qy   446 ENQP-------YNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFL-WFY 497
         ::| |       |||: | ||  ::| | |||| ||:| |:|||:|| ||| | |||
Db   60 EIYPPEVAEFVY-------ITDDTYTKKQVLRMEHLVLKVLTFDLAAPTVNQFLTQYF 110

Qy   498 LKAARANPEVERKAKSLAVTSLSD-QTQLCFWPSTVAAA 535
         || |||||| ||||  |||||| |  ||| || ||
Db   111 LHQQPANCKVESLAMFLGELSLIDADPYLKYLPSVIAGA 149
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Qy   Query Match           6.2%;     Score 184.5;   DB 2;    Length 404;
;    Best Local Similarity 21.7%;    Pred. No. 2.4e-08;
;    Matches  84;  Conservative  72;  Mismatches 148;  Indels  83;  Gaps  13;
;
Qy   215 ISKPSSFVEA-DSSLGSAKELKPELEIVGCVSDLACSEKFSEEVSDSLDDESSEQRSEIY 273
         ||:|||| |   || || |||| |||| | |||| |||  || |  :|||  |||| | ||
Db   1 MSRSSRLQAKQQPQPSQTESPQEAQII----QAKKRKTTQDVKRREEVTKKHQYEIR  55

Qy   274 SQYSDFDYSDYTPSIFFDSGSEFSEKSSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSC 333
         |  |   | |   ||||:||| :   |   ::   |  || | ||| || |||||| | |
Db   56 NCWPPVLSGGISPCIIIE---TPHKEIGTSD---FSRFTNYRFKNLFINPSPLPDLSWGC 109

Qy   334 EEEIHSELLRFDDEEVEESYLRLRERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQW 393
         ::| ||  ::|: : :| || | |:|||||||  || |  ||||||| | | || ||
Db   110 SKEVWLNLMLKKESRYVHDKHFEVL------------------HSDLEPQMRSILLDW 148

Qy   394 IVKQCSDMGLQQOETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEE-NQPYNS 452
         ::|: ||||| :||:| || || || |:|| |||  ||| |: |:|| |||:  ||||:
Db   149 LLEVCEVYTLHRETFYLAQDFDFRFMLTQKDINKNMLQLIGITSLFIASKLEEIYAP--- 205

Qy   453 IRKRNFTIQNLRY-----SRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLK--AARAN 504
         ::|| | |||||      || |||| ||||:|||| | | ||: ||||| |::  ||||
Db   206 ------KLQEFAYVTDGACSEEDILRMELIILKALKWELCPVTIISWLNLFLQVDALKDA 259

Qy   505 PEVERKAKS-----LAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISA 549
         :|:        |||||||| |:|||| || ||||| ||| ||||||
Db   260 PKVLLPQYSQETFIQIAQLLDLCILAIDSLEFQYRI----LTAAALCHFTSIE----- 308

Qy   550 YQRVIKVHVRTTDNELPECVKSLDWLL 576
         ::| |  : |||| | || |||| ||
Db   309 ---VVKKASGLEWDSISECV--DWMV 329
```

```
Qy   Query Match           6.2%;     Score 184.5;   DB 4;    Length 404;
;    Best Local Similarity 21.7%;    Pred. No. 2.4e-08;
;    Matches  84;  Conservative  72;  Mismatches 148;  Indels  83;  Gaps  13;
;
Qy   215 ISKPSSFVEA-DSSLGSAKELKPELEIVGCVSDLACSEKFSEEVSDSLDDESSEQRSEIY 273
         ||:|||| |   || || |||| |||| | |||| |||  || |  :|||  |||| | ||
Db   1 MSRSSRLQAKQQPQPSQTESPQEAQII----QAKKRKTTQDVKRREEVTKKHQYEIR  55

Qy   274 SQYSDFDYSDYTPSIFFDSGSEFSEKSSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSC 333
         |  |   | |   ||||:||| :   |   ::   |  || | ||| || |||||| | |
Db   56 NCWPPVLSGGISPCIIIE---TPHKEIGTSD---FSRFTNYRFKNLFINPSPLPDLSWGC 109

Qy   334 EEEIHSELLRFDDEEVEESYLRLRERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQW 393
         ::| ||  ::|: : :| || | |:|||||||  || |  ||||||| | | || ||
Db   110 SKEVWLNLMLKKESRYVHDKHFEVL------------------HSDLEPQMRSILLDW 148

Qy   394 IVKQCSDMGLQQOETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEE-NQPYNS 452
         ::|: ||||| :||:| || || || |:|| |||  ||| |: |:|| |||:  ||||:
Db   149 LLEVCEVYTLHRETFYLAQDFDFRFMLTQKDINKNMLQLIGITSLFIASKLEEIYAP--- 205

Qy   453 IRKRNFTIQNLRY-----SRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLK--AARAN 504
         ::|| | |||||      || |||| ||||:|||| | | ||: ||||| |::  ||||
Db   206 ------KLQEFAYVTDGACSEEDILRMELIILKALKWELCPVTIISWLNLFLQVDALKDA 259

Qy   505 PEVERKAKS-----LAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISA 549
         :|:        |||||||| |:|||| || ||||| ||| ||||||
Db   260 PKVLLPQYSQETFIQIAQLLDLCILAIDSLEFQYRI----LTAAALCHFTSIE----- 308

Qy   550 YQRVIKVHVRTTDNELPECVKSLDWLL 576
         ::| |  : |||| | || |||| ||
Db   309 ---VVKKASGLEWDSISECV--DWMV 329
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,694
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McConathy, Evelyn H.
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 0609.4070002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-694-5

Query Match   6.2%; Score 184; DB 2; Length 149;
Best Local Similarity 37.1%; Pred. No. 5.4e-09;
Matches 56; Conservative 25; Mismatches 66; Indels 4; Gaps 3;

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Qy 386 LRSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIE 445
       :|:|:|:|:|:.: |||||||||:||||||||||:|||||.|.|:||..|.|.|.|:||
Db 1   MRCILVDWLVEVSEEDKLHRETLFLGVNYIDRFLSKISVLRGK-LQLVGAASMFLAAKYE 59

Qy 446 ENQPYNSIRKRNFTIQNLRYSRHEVVAMEWLYQEVLNFKCFTPTIFNFLWFYLKAARANP 505
       ||| ||| |.| ||:.|| .|.||||||||||||||||||||:|||:||.|.|:.||:|
Db 60  EIYPPDV--KEFAYITDDTYTSQQVLRMEHLLKVLTFDVAVPTTNWFCEDEFLKSCDADD 117

Qy 506 EVERKAKSLAVTSLSD-QTQLCFWPSTVAAA 535
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Db 118 KLKSLTMFLTELTLIDMDAYLKYLPSITAAA 148
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RESULT 13
US-08-460-744-5
; Sequence 5, Application US/08460744
; Patent No. 6107541
; GENERAL INFORMATION:
; APPLICANT: Arnold, Andrew
; TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,744
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McConathy, Evelyn H.
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 0609.4070005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-744-5

Query Match   6.2%; Score 184; DB 3; Length 149;
Best Local Similarity 37.1%; Pred. No. 5.4e-09;
Matches 56; Conservative 25; Mismatches 66; Indels 4; Gaps 3;

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Qy 386 LRSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIE 445
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Db 1   MRCILVDWLVEVSEEDKLHRETLFLGVNYIDRFLSKISVLRGK-LQLVGAASMFLAAKYE 59

Qy 446 ENQPYNSIRKRNFTIQNLRYSRHEVVAMEWLYQEVLNFKCFTPTIFNFLWFYLKAARANP 505
       ||| ||| |.| ||:.|| .|.||||||||||||||||||||:|||:||.|.|:.||:|
Db 60  EIYPPDV--KEFAYITDDTYTSQQVLRMEHLLKVLTFDVAVPTTNWFCEDEFLKSCDADD 117

Qy 506 EVERKAKSLAVTSLSD-QTQLCFWPSTVAAA 535
       ::|: ||| | || ||| || |||
Db 118 KLKSLTMFLTELTLIDMDAYLKYLPSITAAA 148
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RESULT 14
US-07-667-711B-5
; Sequence 5, Application US/07667711B
; Patent No. 6110700
; GENERAL INFORMATION:
; APPLICANT: ARNOLD, ANDREW
; TITLE OF INVENTION: Prad1 Cyclin and its cDNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/667,711B
; FILING DATE: 11-MAR-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MCPHAIL, DONALD R.
; REGISTRATION NUMBER: 35,811
; REFERENCE/DOCKET NUMBER: 0609.4070000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-07-667-711B-5

Query Match   6.2%; Score 184; DB 3; Length 149;
Best Local Similarity 37.1%; Pred. No. 5.4e-09;
Matches 56; Conservative 25; Mismatches 66; Indels 4; Gaps 3;

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Qy 386 LRSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIE 445
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RESULT 15
US-08-193-977-4
; Sequence 4, Application US/08193977
; Patent No. 5625031
; GENERAL INFORMATION:
;  APPLICANT:  WEBSTER, KEVIN R.
;  APPLICANT:  COLEMAN, KEVIN G.
;  TITLE OF INVENTION:  PEPTIDE INHIBITORS OF THE P33CDK2 AND
;  TITLE OF INVENTION:  P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN
;  TITLE OF INVENTION:  PAPILLOMAVIRUS E7 ONCOPROTEIN
;  NUMBER OF SEQUENCES:  34
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE:  REED & ROBINS
;    STREET:  635 BRYANT STREET
;    CITY:  PALO ALTO
;    STATE:  CALIFORNIA
;    COUNTRY:  UNITED STATES OF AMERICA
;    ZIP:  9430l
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE:  Floppy disk
;    COMPUTER:  IBM PC compatible
;    OPERATING SYSTEM:  PC-DOS/MS-DOS
;    SOFTWARE:  PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  US/08/193,977
;    FILING DATE:  08-FEB-1994
;    CLASSIFICATION:  530
;  ATTORNEY/AGENT INFORMATION:
;    NAME:  ROBINS, ROBERTA L.
;    REGISTRATION NUMBER:  33,208
;    REFERENCE/DOCKET NUMBER:  5998-0016
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  (415) 617-8999
;    TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  173 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-193-977-4

  Query Match             6.2%;  Score 183;  DB 1;  Length 173;
  Best Local Similarity  33.3%;  Pred. No. 8.4e-09;
  Matches   58;  Conservative  25;  Mismatches  69;  Indels  22;  Gaps   5;

Qy     360 ERSHAYWRD------CAKAYCSRMDNTGLIPRLRSIMVGWIVKQCSDMGLQQETLFLGVGLL 415
               |::|:|:     |||||| |:|::  ||:||:||||||||||||||||||||||||
Db       5 EDIHTVLREMEVCKCPKVGYMKKQPDITNSMRAILVDWLVEVGEEYKLQNETLHLAVNYI 64

Qy     416 DRFLSKGSFKSERTLILLVGIASLLTLATRIEENQP------YNSIRKRNFTIQNLRYSRH 468
           |||||::||::| |:|::  ||:|::  |||::       |:||::  |::
Db      65 DRPLSSMSVLRGK-LQLVGTAAMLLASKFEEIYPPEVAEFVY-----IYDDTYYKK 114

Qy     469 EVVAMEWLVQEVLNFKCFTPIIFNFL-WFYLKAARANPEVERKAKSLAVTSLSD 521
           |:|:|:|||||:  |:|:| ||| ||   ::|  |||||||||||||||||||
Db     115 QVLRMEHLVLKVLTFDLAAPTVNQFLTQYFLHQQPANCKVESLAMFLGELSLID 168.

Qy       1 MRCILVDWLVEVSEEDKLHRETLFLGVNYIIDRFLSKISVLRGK-LQLVGAASMFLAAKYE 59
           ::|:| :|:  ::|  :|||||||||||| | |||||||||| :|  ||:| ||:|| |
Db     446 ENQPYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPIIFNFLWFYLKAARANP 505

Qy      60 EIYPPDV--KEFAYITDDTYTSQQVLRMEHLILKVLTFDVAVPTTNWFCEDFLKSCDADD 117
                 :| |  :|  |:::  :|||:| :||:|:| :||||| || ||: : ::   ::
Db     118 KLKSLTMFLTELTLIIDMDAYLKYLPSITAAA 148

Qy     506 EVERKAKSLAVTSLSD-QTQLCFWPSTVAAA 535
           ::|::|| | ||:||  |||| |||||||||
Db     118 KLKSLTMFLTELTLIIDMDAYLKYLPSITAAA 148
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OM protein - protein search, using sw model

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Run on: July 23, 2002, 14:18:10 ; Search time 34.11 Seconds
(without alignments)
1882.165 Million cell updates/sec

Title: US-09-821-839-2
Perfect score: 2952
Sequence: 1 MKEIAMRNSKRKPEPTPPAG..........RTTDNELPECVKSLDWLLGQ 578
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 74574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2952	100.0	578	22	AAE12998	Arabidopsis thalia
2	738	25.0	145	22	AAE12999	Arabidopsis thalia
3	241.5	8.2	424	21	AAB35801	Protein involved i
4	222	7.5	509	21	AAB35800	Protein involved i
5	208.5	7.1	515	21	AAB56707	Human prostate can
6	207	7.0	431	12	AAR13731	Human prostate can
7	198.5	6.7	449	21	AAB35799	Human cyclin A. H
8	196	6.6	420	21	AAB43702	Protein involved i
9	195	6.6	398	20	AAW87566	Human cancer assoc
10	195	6.6	398	22	AAB92927	A cyclin related p
11	194	6.6	295	20	AAY31889	Corn cyclin A part

12	193	6.5	348	21	AAG24671	Arabidopsis thalia
13	193	6.5	360	21	AAG24670	Arabidopsis thalia
14	193	6.5	369	21	AAG24669	Arabidopsis thalia
15	191	6.5	433	17	AAW00365	Human cyclin B1.
16	191	6.5	433	22	AAM38874	Human polypeptide
17	191	6.5	475	22	AAM40660	Human polypeptide
18	191	6.4	490	22	ABB61937	Drosophila melanog
19	188.5	6.4	421	22	ABG09366	Novel human diagno
20	184.5	6.2	404	20	AAY43173	Human cyclin E2 pr
21	184.5	6.2	404	21	AAY77483	Human cyclin E2 pr
22	184.5	6.2	404	22	AAY72462	Human cyclin E2 fu
23	182	6.2	336	22	ABB66872	Drosophila melanog
24	179.5	6.1	403	20	AAY43174	Mouse cyclin E2 pr
25	179.5	6.1	403	22	AAY72463	Mouse cyclin E2 fu
26	175	5.9	350	21	AAG14334	Arabidopsis thalia
27	175	5.9	372	21	AAG14333	Arabidopsis thalia
28	175	5.9	399	21	AAG14332	Arabidopsis thalia
29	173.5	5.9	709	22	ABB60267	Drosophila melanog
30	173.5	5.9	709	22	ABB60289	Drosophila melanog
31	168.5	5.7	339	20	AAX31894	Soybean cyclin del
32	168.5	5.7	411	16	AAR77416	Schizosaccharomyce
33	168	5.7	492	18	AAW01560	CYB1 protein. Can
34	168	5.7	492	21	AAX15117	Candida cyclin, CY
35	166.5	5.6	387	21	AAG29315	Arabidopsis thalia
36	161.5	5.5	227	21	AAG29316	Arabidopsis thalia
37	161.5	5.5	339	21	AAG29788	Arabidopsis thalia
38	160.5	5.4	602	22	ABB66407	Drosophila melanog
39	159	5.4	575	22	ABB61825	Drosophila melanog
40	158	5.4	328	21	AAG29789	Arabidopsis thalia
41	155.5	5.3	295	13	AAR27114	prad1. Homo sapie
42	155.5	5.3	295	15	AAR54044	bcl-1 protein. Ho
43	155.5	5.3	295	22	AAB90768	Human shear stress
44	155.5	5.3	618	18	AAW18571	Human cyclin D1-hu
45	155.5	5.3	618	19	AAW74572	Human cyclin D1/cy

ALIGNMENTS

RESULT 1
AAE12998

ID AAE12998 standard: Protein; 578 AA.
XX
AC AAE12998;
XX
DT 28-JAN-2002 (first entry)
XX
DE Arabidopsis thaliana SDS protein.
XX
KW Meiotic prophase I; chromosome 1; male sterile SDS mutant; apomixis;
KW plant breeding; seed production; SDS protein.
XX
OS Arabidopsis thaliana.
XX
PN WO200174144-A1.
XX
PD 11-OCT-2001.
XX
PF 29-MAR-2001; 2001WO-US09875.
XX
PR 31-MAR-2000; 2000US-193523P.
XX
PA (UYPE-) UNIV PENNSYLVANIA STATE.
XX
PI Ma H;
XX
DR WPI; 2001-662939/76.
DR N-PSDB; AAD21310.
XX
FH Key Location/Qualifiers
FT Domain 361..521
FT /label= Cyclin_domain

PT A new plant gene from Arabidopsis, designated SDS, mutations in which
PT are associated with inability to produce pollen, is useful for the
PT production of male sterile plants for plant breeding -
XX
PS Claim 7; Fig 1; 47pp; English.
XX
CC The patent discloses novel plant gene from Arabidopsis thaliana,
CC designated SDS, which is associated with a failure to maintain
CC homologue attachment during meiotic prophase I. The SDS gene is
CC located on chromosome 1 and is useful in plant breeding to produce
CC male sterile SDS mutants and cloned progeny by apomixis where
CC meiosis is bypassed in seed production. The gene may also be
CC used as a probe to identify related genes in other plant species,
CC and to identify and isolate other genes of the meiosis regulatory
CC pathway. The present sequence is SDS protein from Arabidopsis thaliana.
XX
SQ Sequence 578 AA;
XX

Query Match   100.0%; Score 2952; DB 22; Length 578;
Best Local Similarity 100.0%; Pred. No. 3.3e-244;
Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MKEIAMRNSRKPEPTPFAGKKLRSTRLRRKRRAQISPVLVQSPLWSKQIGVSAASVDSCS 60
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db      1 mketamrnsrkpeptpfagkklrstrlrrkraqispvlvqgsplwskqigvsaasvdscs 60

Qy     61 DLLADDNVSCGSSRVEKSSNPKKTLIEEVEVSVSKPGTVNKEITGDSKFPRITRSYSKLHKE 120
          ||||||||||||||||||||||||||||||| |||| |||||||||| ||||||||| |||
Db     61 dlladdnvscgssrvekssnpkktlieevevskpgynvketigdskfritrsyskhke 120

Qy    121 KEGDEIEVSESSCVDSNSGAGLRRLNVKGNKINDNDEISFSRSDVTPAGHVSNSRSLNFE 180
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    121 kegdeievsesscvdsnsgaglrrlnvkgnkindndeisfsrsdvtfaghvsnsrslnfe 180

Qy    181 SENKESDVVSVSIGVEYCSKPGSVTGGADNEEIEISKPSSFVEADSSLGSAKELKPELEI 240
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    181 senkesdvvsvsigvveycskpgsvtggadneeieiskpssfveadsslgsakelkpelei 240

Qy    241 VGCVSDLACSEKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYTPSIFFDSGSSEFSEKS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 vgcvsdlacsekfseevsdslddesseqrseiysqysdfdysdytpsiffdsgssefseks 300

Qy    301 SSDSPISHSRSLYLQPKEQFCRSTIPNDFGSSCEEEIHSELLRFDDEVEESYLRLRERE 360
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    301 ssdspishsrslylqpkeqfcrstipndfgssceeehsellrfddeveesylrlrere 360

Qy    361 RSHAYMRDCAKAYCSRMDNTGLIPRLRSIMYQWIVKQCSDMGLQOETLFLGVGLLDRFLS 420
          |||||||||||||||||||||||||||||| ||||||||||||| ||||||||||||||
Db    361 rshaymrdcakaycsrmdntgliprlrsimvgwivkqcsdmglqqetlflgvglldrfls 420

Qy    421 KGSFKSERTLILVGIASLTLATRIEENQPYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEV 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 kgsfksertlilvgiasltlatrieenqpynsirkrnftiqnlrysrhevvamewlvqev 480

Qy    481 LNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVIA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 lnfkcftptifnflwfylkaaranpeverkakslavtslsdqtqlcfwpstvaaalvvia 540

Qy    541 CIEHHKISAYQRVIKVHVHVRTTDNELPECVKSLDWLLGQ 578
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RESULT 2

ID AAE12999 standard; Protein; 145 AA.
XX
AC AAE12999;
XX
DT 28-JAN-2002 (first entry)
XX
DE Arabidopsis thaliana SDS protein cyclin box.

XX
KW Meiotic prophase I; chromosome 1; male sterile SDS mutant; apomixis;
KW plant breeding; seed production; SDS protein; cyclin box.
XX
OS Arabidopsis thaliana.
XX
XX
DR WPI; 2001-662939/76.
XX
PI Ma H;
XX
PN WO20017414A-A1.
XX
PD 11-OCT-2001.
XX
PF 29-MAR-2001; 2001WO-US09875.
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PR 31-MAR-2000; 2000US-193523P.
XX
PA (UYPE-) UNIV PENNSYLVANIA STATE.
XX
PT A new plant gene from Arabidopsis, designated SDS, mutations in which
PT are associated with inability to produce pollen, is useful for the
PT production of male sterile plants for plant breeding -
XX
PS Disclosure; Page 43; 47pp; English.
XX
CC The patent discloses novel plant gene from Arabidopsis thaliana,
CC designated SDS, which is associated with a failure to maintain
CC homologue attachment during meiotic prophase I. The SDS gene is
CC located on chromosome 1 and is useful in plant breeding to produce
CC male sterile SDS mutants and cloned progeny by apomixis where
CC meiosis is bypassed in seed production. The gene may also be
CC used as a probe to identify related genes in other plant species,
CC and to identify and isolate other genes of the meiosis regulatory
CC pathway. The present sequence is Arabidopsis thaliana SDS protein
CC cyclin box.
XX
SQ Sequence 145 AA;
XX

Query Match   25.0%; Score 738; DB 22; Length 145;
Best Local Similarity 100.0%; Pred. No. 2.6e-55;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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          |||||||||||||| ||||||||||||| ||||||||||||||||||||||||||||||
Db      1 mdntgliprlrsimvgwivkqcsdmglqqetlflgvglldrflskgsfksertlilvgia 60

Qy    437 SLTLATRIEENQPYNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWF 496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sltlatrieenqpynsirkrnftiqnlrysrhevvamewlvqevlnfkcftptifnflwf 120

Qy    497 YLKAARANPEVERKAKSLAVTSLSD 521
          |||||||||||||||||||||||||
Db    121 ylkaaranpeverkakslavtslsd 145
```

RESULT 3

ID AAB35801 standard; Protein; 424 AA.
XX
AC AAB35801;
XX
DT 23-FEB-2001 (first entry)
XX
DE Protein involved in cell cycle regulation SEQ ID 30.

XX
KW Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
KW cotton; rice; barley; millet.
OS zea mays.

```
PN   WO200065040-A2.
XX
PD   02-NOV-2000.
XX
PF   13-APR-2000; 2000WO-US09975.
XX
PR   22-APR-1999;   99US-0130849.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Helentjaris TG, Habben JE, Sun Y;
XX
DR   WPI; 2000-687333/67.
DR   N-PSDB; AAC83108.
XX
PS   Claim 16; Page 106-107; 122pp; English.
XX
PT   Nucleic acids useful for producing transgenic plants, preferably maize,
PT   with increased cell cycle gene activity, preferably activity of cyclin
PT   and/or cyclin-dependent kinase -
XX
CC   Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
CC   AAB35806 which are involved in regulating the cell cycle. The protein and
CC   DNA sequences have been isolated from Zea mays (corn), and the invention
CC   also includes oligonucleotides. The cell cycle polynucleotide sequences
CC   are useful for producing transgenic plants such as maize, soybean,
CC   sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
CC   millet with increased levels of cell cycle gene activity, such as
CC   activity of cyclin and cyclin-dependent kinases. The DNA sequences are
CC   also useful as probes for detecting deficiencies in the level of mRNA in
CC   screening for desired transgenic plants, for detecting mutations in the
CC   gene, for monitoring upregulation of expression or changes in enzyme
CC   activity, for screening assays of compounds, for detecting any number of
CC   allelic variants, orthologs or paralogs of the gene, and site-directed
CC   mutagenesis in eukaryotic cells. The DNA sequences are also useful for
CC   recombinant expression of the encoded polypeptides and as immunogens for
CC   preparing and screening antibodies. A transgenic plant comprising an
CC   expression cassette including a cell cycle regulatory gene is useful for
CC   assaying enzyme agonists and antagonists, and as immunogens or antigens
CC   to obtain antibodies. The antibodies are useful in assaying expression
CC   levels of cell cycle regulatory proteins, for identifying and isolating
CC   nucleic acids from expression libraries, for identifying homologues of
CC   polypeptides from other species, and for purification of the proteins.
XX
SQ   Sequence    424 AA;

Query Match             8.2%;   Score 241.5;  DB 21;   Length 424;
Best Local Similarity  24.4%;   Pred. No. 5.3e-12;
Matches   85;  Conservative   65;  Mismatches  140;  Indels   59;  Gaps    9;

Qy   231 AKELKPELE-IVGCVSDLACSEKFSEEVSDSLDDESSEQSEIYSQYSDFDYSDYYPSIF 289
             | :||  | :|| ||  ::| :| : ||||| ||:   :|  ||::|  |||
Db    79 askqpecqpivadpepevcqqk--esvgdqtvdivdivgdsdsddmgatenkdi 136

Qy   290 FDSGSEFSEKSSSDS--PIS---HSRSLYLQFKEQFCRSTIPNDFGSSCEEIHSELLRF 344
             |:|| || |  :|    |      |  :||||:   |:::|::   ||:  |:|::
Db   137 mnedellmdidsadsgnplaateyvkelytfyreneaksovrpdymss-qqdins---- 190

Qy   345 DDEEVEESYLRLRERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQ 404
                 ::|:|::  || :|:| | :: |  | ||  : | | |:| |
Db   191 ------------------------kmrallidwjlievhykfelm 210

Qy   405 QETLFLGVGLLDRFLSKGSFKSERTLLILVGIASLTLATRIEE-NQPYNSIRKRNFTIQNL 463
              :|:|:| ||:|: ::||| :: || :|  | :: | ||
Db   211 detlflmvnlidrfiek-evvprkhlqvgvtamllackyeevsvp--vvedlvlisdr 266

Qy   464 RYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLWFYLKAARANPEVERKAKSLAVTSLSDQT 523
              |||| ||  || | |  | | |  |  |  : | : | :| | |:
Db   267 aytkgqilemeklllntlgfnmsvptpyvfmkrflkaadadkqlelasffmlelclveyq 326

Qy   524 QLGFWPSTVAALVVLACIEHNKISAYQRVIKVHVHVRTTDNELPECVKSL 572
```

```
Db   327 mlnyrpshlaaaavytaqgeainrcqhwtkvceeshsrytsdqllecsrmm 375


RESULT   4
AAB35800
ID   AAB35800 standard; Protein; 509 AA.
XX
AC   AAB35800;
XX
DT   23-FEB-2001  (first entry)
XX
DE   Protein involved in cell cycle regulation SEQ ID 26.
XX
OS   Zea mays.
XX
XX
PN   WO200065040-A2.
XX
PD   02-NOV-2000.
XX
PF   13-APR-2000; 2000WO-US09975.
XX
PR   22-APR-1999;   99US-0130849.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Helentjaris TG, Habben JE, Sun Y;
XX
DR   WPI; 2000-687333/67.
DR   N-PSDB; AAC83107.
XX
PS   Claim 16; Page 103-104; 122pp; English.
XX
PT   Nucleic acids useful for producing transgenic plants, preferably maize,
PT   with increased cell cycle gene activity, preferably activity of cyclin
PT   and/or cyclin-dependent kinase -
XX
CC   Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
CC   AAB35806 which are involved in regulating the cell cycle. The protein and
CC   DNA sequences have been isolated from Zea mays (corn), and the invention
CC   also includes oligonucleotides. The cell cycle polynucleotide sequences
CC   are useful for producing transgenic plants such as maize, soybean,
CC   sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
CC   millet with increased levels of cell cycle gene activity, such as
CC   activity of cyclin and cyclin-dependent kinases. The DNA sequences are
CC   also useful as probes for detecting deficiencies in the level of mRNA in
CC   screening for desired transgenic plants, for detecting mutations in the
CC   gene, for monitoring upregulation of expression or changes in enzyme
CC   activity, for screening assays of compounds, for detecting any number of
CC   allelic variants, orthologs or paralogs of the gene, and site-directed
CC   mutagenesis in eukaryotic cells. The DNA sequences are also useful for
CC   recombinant expression of the encoded polypeptides and as immunogens for
CC   preparing and screening antibodies. A transgenic plant comprising an
CC   expression cassette including a cell cycle regulatory gene is useful for
CC   assaying enzyme agonists and antagonists, and as immunogens or antigens
CC   to obtain antibodies. The antibodies are useful in assaying expression
CC   levels of cell cycle regulatory proteins, for identifying and isolating
CC   nucleic acids from expression libraries, for identifying homologues of
CC   polypeptides from other species, and for purification of the proteins.
XX
SQ   Sequence    509 AA;

Query Match             7.5%;   Score 222;  DB 21;   Length 509;
Best Local Similarity  26.4%;   Pred. No. 3.3e-10;
Matches  105;  Conservative   74;  Mismatches  157;  Indels   64;  Gaps   20;

Qy   203 SVTGGADNEIEISKPSSFVEAD--SSLGSAKEL----KPELEIVGCVSD-----LACS 250
```

```
Db    96  sirgsad------kpasikpappvazhgsatgrhnvpppkvptiadvpsrapalvsct  148
          !:|!|           !:|| !    !:|           !:||
Qy   251  EKFSEEVS-DSLDDESSEQRSEIYSQYS-DFDYSDYTPSIFFDSGSEFSEKSSSDSPISH  308
          !!|:||| !| |       !||:||    !||  |!   ||           ||
Db   149  glvspgrsgdsv--ssdetmstcdsmkspdfeyvdnqdtsmlas---lqrtsehlrise  203
          !!  :|  |!      !   |  :|||  ||  !|           || !
Qy   309  SRSLYLQFKEQPCRSTIPNDFGSSCCEEIHSELLRFDDEEV-----EESYLRLERER--  361
          !:|: ||       :: ||    |!     |!:  |||:||     |!|| |||:|
Db   204  drdveenkrkk-navapmeidric--dvdse---yedpqcatiasdiymhireaetkk  256
          |   ||||  !   :|  !      !|: |!  ||
Qy   362  --SHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQOETLFLGVGLLDRFL  419
          |  |!| !     |:|! ||  |!|   :|  :|!|   !|  | !|||:|||!||||
Db   257  rpstdfmetiqk--------dvnpsmrailldwlveyaeeyrlvpdtlyltvnyidryl  307
          || !|     !        ||    !| ||:|| !   ||| |   |: |!!|:|
Qy   420  SKGSFKSERTLILVGIASLTLATRIEENQPYNSIRKRNFT-IQNLRYSRHEVVAMEWLVQ  478
          :||||!    |||||!|||||| |||!||||       ||| |||||||||||||!||
Db   308  s-gneisrqrlglgvacmliaakyee---lcapqveefcyitdntyfrdevidmeasvl  363
          :      |:|   |! |!|      ||       | !!  | !    !:  | ||
Qy   479  EVLNFKCFTPTIPNFLWFYLKAARANPE-------VERKAKSLAVTSLSDQTQLCFWPSTVA  533
          |!||||  |!    || | !! !| ||        |||||||||||||| !!    ||||
Db   364  nylkfemtaptakcflrrfaraaqacdedpalhleflanylaelslleyslisyppslia  423
          |! ||           !|    !  | |        | |||:  !  |||:|!|:|||!
Qy   534  AALVVLA--CIEHNKISAYQRVIKVHVHVRTTDNELPECVKSL  572
          ||||||| | !!|!!|:  |! !|! ||:|| |: | |||||
Db   424  asaiflarfllgptky-pwnstlahytqykpskisecvkal  463
```

CC   nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC   and can be used in gene therapy. The prostate cancer antigen
CC   polynucleotides may be used for detection of prostate cancer, chromosome
CC   identification, as chromosome markers, and for numerous other diagnostic
CC   or research purposes. The prostate cancer antigens may be used to treat
CC   disorders such as neural, immune, muscular, reproductive,
CC   gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC   disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC   AAB57303 represent sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 515 AA;

RESULT 6

ID   AAR13731 standard; Protein; 431 AA.
XX
AC   AAR13731;
XX
DT   07-NOV-1991 (first entry)
XX
DE   Human cyclin A.
XX
KW   Tumour; cancer; Hepatitis B virus; cell proliferation; hepatitis;
KW   cirrhosis; hyperleucocytic acute myeloblastic leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO9112324-A.
XX
PD   22-AUG-1991.
XX
PF   06-FEB-1991; 91WO-FR00089.
XX
PR   12-FEB-1990; 90FR-0001596.
XX
PA   (INRM) INSERM INST NAT SANTE.
XX
PI   Brechot C, Wang J, Henglein B, Zindy F;
XX
DR   WPI; 1991-267135/36.
DR   N-PSDB; AAQ13385.
XX

```
Query Match             7.1%;   Score 208.5;   DB 21;   Length 515;
Best Local Similarity  24.6%;   Pred. No. 4.8e-09;
Matches    88;  Conservative  65;  Mismatches 126;  Indels  79;  Gaps  13;

Qy   214  EISKPSSFVEADSSLGSAKELKPELEIVGCVSDLACSEKF------SEEVSDSLD-D  263
          |!:!|:  |! |!   :  | || |!  | !      |:         :||| ||| |
Db   137  evrepa------gssaqrpktrrvapikdlpvndehvtvppwkanskqpaftlhvd  187

Qy   264  ESSEQRSEIYSQYSDFDYSDYTPSIFFDSG------------SEFSEKSSSDSPISHSRS  311
          |:|:|| !:|:|  |:||  |:| ||||            !|:|:| || ::|| ||
Db   188  eaekeeagkkpaessqklered--alafnsaislpggrtkplvpldypmdgsfesphtmdms  244

Qy   312  LYLQFKEQPCRSTIPNDFGSSCCEEIHSELLRFDDEEVEESYLRLRERERSHAYMRDCAK  371
          |!| !|!      : !|!!    |    |!|  |  !   !:   | :|   |  |
Db   245  ivledekpvsvnevpd-----yhedih--------------tylremevk------ckp  278

Qy   372  AYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQOETLFLGVGLLDRFLSKGSFKSERTLI  431
          | |:|!|| ||  |!|!|!|  :|  !|  |||      !|!||||||| |   |||||!
Db   279  kvgymkkqpditnsmraiivdwlvevgeeykiqnetihlavnyidrflssmsvlrgk-lq  337

Qy   432  LVGIASLTLATRIEENQP-----YNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFK  484
          |||||||||||||||||       |||||||!||||||||||||||||||||||!||||
Db   338  lvgtaamllaskfeelyppevaefvy------ltddtytkkqvirmehlvlkvltfd  388

Qy   485  CFTPTIPNFL-WFYLKAARANPEVERKAKSLAVTSLSD-QTQLCFWPSTVAAALVVLA  540
          |  | !| !|  | | !! !!   |:|||||||||||||   ||   |||| ||||||
Db   389  laaptvnqfltqyflhqqpanckves.lamfigelsildadpylkylpsvlagaafhla  446
```

```
PT   New nucleotide sequence encoding human cyclin A - and derived
PT   antibodies and anti-sense DNA, for diagnosis and treatment of
PT   cell proliferation, respectively
XX
PS   Disclosure; Page 15-16; 23pp; English.
XX
CC   The human genome contains (on chromosome 4q27) a specific site for
CC   integration of HBV into the cycline A gene. Such integration
CC   occurs in liver cells at early stages of tumour development without
CC   significant chromosomal rearrangement or histological signs of
CC   hepatitis or cirrhosis. Expression of cycline A is associated with
CC   cell devision so integration of HBV interferes with regulation of
CC   cell multiplication.
CC   Antibodies to cycline A are used to determine the cellular level of
CC   cycline A for diagnosis of cell proliferation. Compsns. contg.
CC   anti-sense cDNA can be used to treat such proliferation (by
CC   blocking cycline A expression). Partic., cycline A is expressed
CC   most highly in hyperleucocytic acute myeloblastic leukaemia during
CC   the period of rapid cell devision and at very low level in primary
CC   liver cancer when the rate of cell devision is low.
XX
SQ   Sequence    431 AA;

Query Match             7.0%;  Score 207;  DB 12;  Length 431;
Best Local Similarity   25.4%;  Pred. No. 4.9e-09;
Matches   87;  Conservative   60;  Mismatches 126;  Indels   70;  Gaps   12;

Qy    229  GSARELKPELEIVGCVSDLACSEKF----------SEEVSDSLID-DESSEQRSEIYSQYSD  278
           | | | |  || |            |          ::| |
Db     59  glaheqrpktrrvapikdlpvndehvtvppwkanskqpattihvdeaekeaqkpaesqk  118

Qy    279  FDYSDYTPSIFFDSG----------SEFSEKSSSDSPISHSRSLYLQFKEQFCRSTIP  326
           :|| | |                  | || :|
Db    119  lered---alafnsaslspggprkplvpldydypmdgsfesphtmdmsivledekpvsnevp  175

Qy    327  NDFGSSCEEIHSELLRFDDEEVEESYLRLRERERSHAYMRDCAKAYCSRMDNTGLIPRL  386
           :|||  ||  || :|| |||  ||   :|                    |
Db    176  d-----yhedih--------tylremevk-------ckpkvgymkkqpditnsm  209

Qy    387  RSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGGSFKSERTLILVGIASLTLATRIEE  446
           |:|:| | |  :||| |: |||  || |  |||  |  ||: |||:|:: || : ||
Db    210  raiivdwivegveegeykklqpetlhlavnyidrflssmsvirgk-lqlvgtaamllaskfee  268

Qy    447  NQP--------YNSIRKRNFTIQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFL-WFYL  498
           | |         |:|  | ||   ||  | ||||:|||| |||| ||  | | :    ||
Db    269  iyppevaefvy-----------ltddtytkgvlrmehlvklvltfdllaaptvnqfltqyfl  319

Qy    499  KAARANPEVERKAKSLAVTSLSD-QTQLGFWPSTVAAALVVLA  540
           | |  | | | ||     ||| |  ::|| | | | ||| ||| |
Db    320  hqgpenckveslamflgelsliidadpylkylpsviagaafhla  362
```

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RESULT   7

ID   AAB35799 standard; Protein; 449 AA.
XX
AC   AAB35799;
XX
DT   23-FEB-2001  (first entry)
XX
DE   Protein involved in cell cycle regulation SEQ ID 22.
XX
KW   Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
KW   cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
KW   cotton; rice; barley; millet.
OS   Zea mays.
XX
PN   WO200065040-A2.
XX
PD   02-NOV-2000.
XX
```

```
PF   13-APR-2000; 2000WO-US09975.
XX
PR   22-APR-1999;              99US-0130849.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Helentjaris TG, Habben JE, Sun Y;
XX
DR   WPI; 2000-687333/67.
DR   N-PSDB; AAC83106.
XX
PT   Nucleic acids useful for producing transgenic plants, preferably maize,
PT   with increased cell cycle gene activity, preferably activity of cyclin
PT   and/or cyclin-dependent kinase -
XX
PS   Claim 16; Page 99-100; 122pp; English.
XX
CC   Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
CC   AAB35806 which are involved in regulating the cell cycle. The protein and
CC   DNA sequences have been isolated from Zea mays (corn), and the invention
CC   also includes oligonucleotides AAC83114 - AAC83139 which are related to
CC   the cell cycle polynucleotides. The cell cycle polynucleotide sequences
CC   are useful for producing transgenic plants such as maize, soybean,
CC   sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
CC   millet with increased levels of cell cycle gene activity, such as
CC   activity of cyclin and cyclin-dependent kinases. The DNA sequences are
CC   also useful as probes for detecting deficiencies in the level of mRNA in
CC   screening for desired transgenic plants, for detecting mutations in the
CC   gene, for monitoring upregulation of expression or changes in enzyme
CC   activity in screening assays of compounds, for detecting any number of
CC   allelic variants, orthologs or paralogs of the gene, and site-directed
CC   mutagenesis in eukaryotic cells. The DNA sequences are also useful for
CC   recombinant expression of the encoded polypeptides and as immunogens for
CC   preparing and screening antibodies. A transgenic plant comprising an
CC   expression cassette including a cell cycle regulatory gene is useful for
CC   assaying enzyme agonists and antagonists, and as immunogens or antigens
CC   to obtain antibodies. The antibodies are useful in assaying expression
CC   levels of cell cycle regulatory proteins, for identifying and isolating
CC   nucleic acids from expression libraries, for identifying homologues of
CC   polypeptides from other species, and for purification of the proteins.
XX
SQ   Sequence    449 AA;

Query Match             6.7%;  Score 198.5;  DB 21;  Length 449;
Best Local Similarity   23.4%;  Pred. No. 2.8e-08;
Matches   83;  Conservative   70;  Mismatches 136;  Indels   65;  Gaps   13;

Qy    231  AKELKPELEIVGCVSDLACSEKFSEEVSDSLDDSSEQRSEIYSQYSDFDYSDYTPSIFF  290
           | ||| || || ||| |: |  |: :| | | :||  || :  : ||  :   |  ||
Db    110  akpppe-dvivlssd------seqsrtqlessassvisr----------kkvin  147

Qy    291  DSGGSEFSEKSSSDSPISHSRSLYLQFKEQFCRSTIPNDFGSSCEEIHSELLRFDDEEVE  350
           :| | :|| | |  :|| : | |      |      ||||  || ||  || || |||
Db    148  tlssvlsarskaacgitdkrr----------qvaviedid--kidvnnelavveyiedi  194

Qy    351  ESYLRLRERERSHAYMRDCAKAYCSRMD-NTGLIPRLRSIMVQWIVKQCSDMGLQQETLF  409
           :|  |  |:  | |||| |||: ||||     |||  | |:|:|||  || |  || ||
Db    195  ytfykiaqhdrrp----------cdyidtqveinpkmrallagwilevhhkfelmpetly  244

Qy    410  LGVGLLDRFLSKGGSFKSERTLILVGIASLTLATRIEE--NQPYNSIRKRNFTIQNLRYSR  467
           | |: | ||| |  | ||  | |||:|:| | || |||       |:| | || ||  ||
Db    245  ltnyiidqylslqpv-lrrelqlvgvsamliackyeeiwapevndf---illsdsaysr  299

Qy    468  HEVVAMEWLVQEVLNFKCFTPTINFLWFYLKAARANPEVERKAKS------LAVTSLS  520
           :: :| |: | || | | | : |  :|| | :| | |              |: ||||
Db    300  eqilsmekgiinslewnltvptvymflvrfikaaalgnkvekemenmvffaelalmqyg  359

Qy    521  DQTQLGFWPSTVAAALVVLACIEHNKISAYQRVIKVHV--RTTDNELPECVKSL  572
           |:| :|  |||||||| ||: ::|                :|    | |  | ||
Db    360  lvtl---pslvaasvyyaarltlkraplvtdtlkhhtgfresecteliec

kll  410
```

RESULT 8
ID   AAB43702 standard; Protein; 420 AA.
XX
AC   AAB43702;
XX
DT   08-FEB-2001 (first entry)
XX
DE   Human cancer associated protein sequence SEQ ID NO:1147.
XX
KW   Human; cancer associated gene; cancer antigen; detection; cancer;
KW   diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
KW   antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW   antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW   dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW   vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW   immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW   allergic reaction; graft versus host disease; organ rejection;
KW   haemostatic; thrombolytic; cardiovascular disorder; infection;
KW   neurological disease; drug screening.
XX
OS   Homo sapiens.
XX
PN   WO200055350-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05882.
XX
PR   12-MAR-1999; 99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Ruben SM;
XX
DR   WPI; 2000-587533/55.
DR   N-PSDB; AAC77911.
XX
PT   Novel isolated nucleic acids comprising sequences encoding peptides
PT   useful for treating or diagnosing e.g. cancer -
XX
PS   Claim 11; Page 1763-1764; 2352pp; English.
XX
CC   AAC77607 to AAC78448 encode the human cancer associated proteins given
CC   in AAB43398 to AAB44239. The proteins can have activities based on the
CC   tissues and cells the genes are expressed in. Example of activities
CC   include: cytostatic; proliferative; vulnerary; immunomodulator;
CC   antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC   antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC   dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC   nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC   polynucleotides and polypeptides can be used for preventing, treating or
CC   ameliorating medical conditions and diagnosing pathological conditions.
CC   Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC   the present invention may be used to treat immune disorders by activating
CC   or inhibiting the proliferation, differentiation or mobilisation of
CC   immune cells, to treat disorders of haematopoietic cells, autoimmune
CC   disorders, allergic reactions, graft versus host disease and organ
CC   rejection, modulate haemostatic or thrombolytic activity, modulate
CC   inflammation, cancers, cardiovascular disorders, neurological disease and
CC   bacterial or viral infections. The peptides, nucleotides, antibodies,
CC   agonists and antagonists may be also be used in drug screens. AAC78449 to
CC   AAC78457 and AAB44240 represent sequences used in the exemplification of
CC   the present invention.
XX
SQ   Sequence   420 AA;

Query Match   6.6%; Score 196; DB 21; Length 420;
Best Local Similarity   31.7%; Pred. No. 4.1e-08;
Matches   63; Conservative 38; Mismatches 88; Indels 10; Gaps   5;

Qy   377 MDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIA 436

Db   178 ldgrdingrmzailvdwilvqvhbskfxilgetlymcvgimdrflqvqpv-srkklqlvgit 236
               :|:   : ||:|:| |:|: |:|| |:|: | |||||| ::| |:|||
Qy   437 SLTLATRIEENQPYNSIRKRNPT-IQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLW 495
               -:||::||: | | |:|:: ||:|:||:|||||:||||||:||||||:||||:|||||
Db   237 alllaskyeemfspnl---edfvyitdnaytssqiremettlikelkfelgrtplphfir 293
               |:|||||||||: | :| ||: :||:|||:||:||:|||||:||:||:|:
Qy   496 FYLKAARANPEVERKAKSLAVTSLSDQTQLGEFWPSTVAAALVVLACIEHNKISAYQRVIK 555
               | |||| ||||| |:| |: ||| | |:|| : || ||::||| |::| :| |:|||
Db   294 raskagevdveqhtlakylmeltlidydmvhyhpskvaaa---asclsqkvlgggkwnlk 350
               |:|| | :|| ||||||||||:| |:||| |:||:| | |:|| |||||| |||
Qy   556 VHVRT--TDNELPECVKSL 572
               ||:|| :| :|| :||:|
Db   351 qqyytgytenevlevmghm 369

RESULT 9
ID   AAW87566 standard; Protein; 398 AA.
XX
AC   AAW87566;
XX
DT   05-MAR-1999 (first entry)
XX
DE   A cyclin related protein HCRP-2.
XX
KW   Human cyclin related protein; HCRP; HCRP-2; cancer; adenocarcinoma;
KW   leukaemia; immune disorder; AIDS; asthma; developmental disorder;
KW   renal tubular acidosis; cerebral palsy.
XX
OS   Homo sapiens.
XX
PN   WO9855510-A2.
XX
PD   10-DEC-1998.
XX
PF   05-JUN-1998; 98US-0870143.
XX
PR   05-JUN-1997; 97US-0870143.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Cocks BG, Corley NC, Guegler KJ, Hillman JL, Shah P;
XX
DR   WPI; 1999-045731/04.
DR   N-PSDB; AAV83711.
XX
PT   Human cyclin related protein, HCRP - useful, e.g. to diagnose and
PT   treat cancer, immune disorders and developmental disorders and
PT   screen for antagonists used to treat cancer
XX
PS   Claim 19; Fig 2A-F; 80pp; English.
XX
CC   The present sequence represents a human cyclin related protein (HCRP)
CC   designated HCRP-2 HCRP Proteins can be used to treat cancer e.g.
CC   adenocarcinoma, leukaemia, etc. or immune disorders e.g. AIDS,
CC   asthma. They can also be used to treat developmental disorders,
CC   e.g. renal tubular acidosis, cerebral palsy. HCRP-2 was expressed in
CC   cancerous and foetal tissues, and increased expression was proposed to
CC   be associated with cancer and decreased expression with developmental
CC   disorders. HCRP can be used to screen for agonists (useful to treat
CC   conditions as above) or antagonists. It can be used to generate
CC   antibodies, useful as antagonists or to diagnose conditions characterised
CC   by HCRP expression and to monitor therapeutic interventions.
CC   Polynucleotides encoding HCRP can be used to detect polynucleotides
CC   encoding HCRP, e.g. to diagnose diseases relating to polypeptide
CC   expression or monitor HCRP regulation during therapeutic intervention.
CC   They are useful to produce complementary or antisense sequences for
CC   therapeutic administration to modulate or prevent HCRP expression e.g. to
CC   treat or prevent cancers as above.
XX
SQ   Sequence   398 AA;

Qy 377 MDNTGLIPRLRSIMVQWIVKQCGSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIA 436
            |:||:||||:|:||:| :|||||:||||||||||||:||||||:|::|||||||||||||||
Db 156 ldgrdingrmralivdwivqvhskfrilgetlymcvgindrflgvqpv-srkklqlvgit 214

Qy 437 SLTLATRIEENQPYNSIRKRNFT-IQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLW 495
            |:|:|||| | |:::|||| |||::|||::||:||||:|::|||
Db 215 alllaskyeemfspni---edfvyltdnaytssqiremetlilkelkfelgrplphflr 271

Qy 496 FYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISAYQRVIK 555
            :||: |||||:||:||||||||||||:||||||||||| :|:
Db 272 raskagevdveqhtlakyimeltlidydmvhyhpskvaaa--asclsqkviggkwnlk 328

Qy 556 VHVRT--TDNELPECVKSL 572
            |:||| ::| ||||
Db 329 qqyytgytenevlevmqhm 347

SQ Sequence 398 AA;

RESULT 11
ID   AAY31889 standard; Protein; 295 AA.
XX
AC   AAY31889;
XX
DT   21-DEC-1999 (first entry)
XX
DE   Corn cyclin A partial polypeptide.
XX
KW   Cyclin A; corn; maize; cell cycle; cell division; transgenic plant;
KW   herbicide; plant breeding.
XX
OS   Zea mays.
XX
PN   WO9948486-A2.
XX
PD   30-SEP-1999.
XX
PF   19-MAR-1999;   99WO-US06047.
XX
PR   23-MAR-1998;   98US-0078948.
XX
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI   Cahoon RE, Klein TM, Odell JT, Orozco EM;
XX
DR   WPI; 1999-591036/50.
DR   N-PSDB; AAZ19953.
XX
PT   New isolated plant cyclin genes, used to develop products for use as
PT   herbicides and for developing plant breeding programs -
XX
PS   Claim 1; Page 44-45; 68pp; English.
XX
CC   This is the deduced amino acid sequence of a portion of a corn
CC   cyclin A protein derived from the nucleotide sequence (see AAZ19953)

Query Match   6.6%; Score 195; DB 22; Length 398;
Best Local Similarity   31.7%; Pred. No. 4.6e-08;
Matches   63; Conservative 38; Mismatches 88; Indels 10; Gaps 5;

Qy 377 MDNTGLIPRLRSIMVQWIVKQCGSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIA 436
            |:||:||||:|:||:| :|||||:||||||||||||:||||||:|::|||||||||||||||
Db 156 ldrdingrmralivdwivqvhskfrilgetlymcvgindrflgvqpv-srkklqlvgit 214

Qy 437 SLTLATRIEENQPYNSIRKRNFT-IQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLW 495
            |:|:|||| | |:::|||| |||::|||::||:||||:|::|||
Db 215 allaskyeemfspni---edfvyltdnaytssqiremetlilkelkfelgrplphflr 271

Qy 496 FYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISAYQRVIK 555
            :||: |||||:||:||||||||||||:||||||||||| :|:
Db 272 raskagevdveqhtlakyimeltlidydmvhyhpskvaaa--asclsqkviggkwnlk 328

Qy 556 VHVRT--TDNELPECVKSL 572
            |:||| ::| ||||
Db 329 qqyytgytenevlevmqhm 347

RESULT 10
ID   AAB92927 standard; Protein; 398 AA.
XX
AC   AAB92927;
XX
DT   26-JUN-2001 (first entry)
XX
DE   Human protein sequence SEQ ID NO:11580.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000;   2000JP-0118776.
PR   02-MAY-2000;   2000JP-0183767.
PR   09-JUN-2000;   2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI   Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 11580; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of

Query Match   6.6%; Score 195; DB 20; Length 398;
Best Local Similarity   31.7%; Pred. No. 4.6e-08;
Matches   63; Conservative 38; Mismatches 88; Indels 10; Gaps 5;

Qy 377 MDNTGLIPRLRSIMVQWIVKQCGSDMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIA 436
            |:||:||||:|:||:| :|||||:||||||||||||:||||||:|::|||||||||||||||
Db 156 ldgrdingrmralivdwivqvhskfrilgetlymcvgindrflgvqpv-srkklqlvgit 214

Qy 437 SLTLATRIEENQPYNSIRKRNFT-IQNLRYSRHEVVAMEWLVQEVLNFKCFTPTIFNFLW 495
            |:|:|||| | |:::|||| |||::|||::||:||||:|::|||
Db 215 alllaskyeemfspni---edfvyltdnaytssqiremetlilkelkfelgrplphflr 271

Qy 496 FYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLACIEHNKISAYQRVIK 555
            :||: |||||:||:||||||||||||:||||||||||| :|:
Db 272 raskagevdveqhtlakyimeltlidydmvhyhpskvaaa--asclsqkviggkwnlk 328

Qy 556 VHVRT--TDNELPECVKSL 572
            |:||| ::| ||||
Db 329 qqyytgytenevlevmqhm 347

```
CC   of a contig composed of clones isolated from corn endosperm
CC   and mesocotyl cDNA libraries.  It represents 80% of the protein
CC   (the C-terminal region).  The invention relates to isolated nucleic
CC   acid fragments (see AAZi9953-66) encoding cyclin A, cyclin delta-1,
CC   cyclin delta-2 and cyclin delta-3 polypeptides (see AAY31889-902).
CC   It also relates to the construction of chimeric genes encoding all
CC   or a portion of a cyclin, in sense or antisense orientation, where
CC   expression of the chimeric gene results in altered levels of the
CC   cyclin protein in a transformed host cell.  This would have the
CC   effect of altering the regulation of cell division in those cells.
CC   The nucleic acid fragments may be used to express cyclins in plant
CC   cells to enhance cell tissue culture growth.  The availability of
CC   nucleic acid sequences encoding all or a portion of cyclins should
CC   facilitate studies of cell cycle in plants, provide genetic tools
CC   to enhance cell growth in tissue culture, increase the efficiency
CC   of gene transfer and help provide more stable transformations.  The
CC   proteins can be used as targets to facilitate design and/or
CC   identification of inhibitors of those enzymes that may be useful as
CC   herbicides.
XX
SQ   Sequence   295 AA;

Query Match             6.6%;  Score 194;  DB 20;  Length 295;
  Best Local Similarity   28.2%;  Pred. No. 3.5e-08;
  Matches   67;  Conservative   51;  Mismatches   84;  Indels   36;  Gaps   9;

Qy        352 SYLRLRERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLG 411
                  ||| ||  |:|  |||:|| ::|:||||: ||:|: |: |
Db         31 tylrslevdpqrrsrsdyieav----qadvtahmrsilvdwlveveaeeyklvadtlylt 85

Qy        412 VGLLDRFLSKGSFKSERTLILVGIASLTLATRIEENQPYNSIRKRNFT-IQNLRYSRHEV 470
                  :|||| | |:||:   |||::|  :||:|  |  ::  :   |: ||
Db         86 lsyvdrflsvnalgrdk-lqllgvasmliaakfeeispph--pedfcyltdntytkeel 141

Qy        471 VAMEWLVQEVLNFKCFTPTIENFLWFYLKAARANPE----VERKAKSLAVTSLSDQTQL 525
                  :| | ||||:  |::|| |:| ||:|  |:|| | |
Db        142 lkmesdikilkfelgnptiktflrrfiirsahedkkgsilmeflgsylaelslldygcl 201

Qy        526 CFWPSTVAAALVVLA-CIEHN------------KISAYQRVIKVHVRTTDNELFECVKSL 572
                  |  |  || |:||     ||   :|      ||    :||  ||
Db        202 rflpsvvaasvmfvarpdidpntnpvwntklqkmtgy---kv------selkdcival 249
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RESULT 12
AAG24671

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ID   AAG24671 standard; protein; 348 AA.
XX
AC   AAG24671;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 28436.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999; 99US-0121825.
PR   05-MAR-1999; 99US-0123180.
PR   09-MAR-1999; 99US-0123548.
PR   23-MAR-1999; 99US-0125788.
PR   25-MAR-1999; 99US-0126264.
PR   29-MAR-1999; 99US-0126785.
PR   01-APR-1999; 99US-0127462.
PR   06-APR-1999; 99US-0128234.
PR   08-APR-1999; 99US-0128714.
PR   16-APR-1999; 99US-0129845.
PR   19-APR-1999; 99US-0130077.
PR   21-APR-1999; 99US-0130449.
PR   23-APR-1999; 99US-0130510.
PR   23-APR-1999; 99US-0130951.
PR   28-APR-1999; 99US-0130891.
PR   28-APR-1999; 99US-0131449.
PR   30-APR-1999; 99US-0132048.
PR   30-APR-1999; 99US-0132207.
PR   04-MAY-1999; 99US-0132404.
PR   05-MAY-1999; 99US-0132485.
PR   05-MAY-1999; 99US-0132486.
PR   06-MAY-1999; 99US-0132487.
PR   07-MAY-1999; 99US-0132663.
PR   11-MAY-1999; 99US-0134256.
PR   14-MAY-1999; 99US-0134218.
PR   14-MAY-1999; 99US-0134219.
PR   14-MAY-1999; 99US-0134221.
PR   14-MAY-1999; 99US-0134370.
PR   18-MAY-1999; 99US-0134768.
PR   19-MAY-1999; 99US-0134941.
PR   20-MAY-1999; 99US-0135124.
PR   24-MAY-1999; 99US-0135353.
PR   25-MAY-1999; 99US-0135629.
PR   27-MAY-1999; 99US-0136021.
PR   28-MAY-1999; 99US-0136782.
PR   01-JUN-1999; 99US-0137222.
PR   03-JUN-1999; 99US-0137528.
PR   04-JUN-1999; 99US-0137502.
PR   07-JUN-1999; 99US-0137724.
PR   08-JUN-1999; 99US-0138504.
PR   10-JUN-1999; 99US-0138540.
PR   10-JUN-1999; 99US-0138847.
PR   14-JUN-1999; 99US-0138919.
PR   16-JUN-1999; 99US-0139919.
PR   16-JUN-1999; 99US-0139433.
PR   17-JUN-1999; 99US-0139992.
PR   18-JUN-1999; 99US-0139956.
PR   18-JUN-1999; 99US-0139454.
PR   18-JUN-1999; 99US-0139455.
PR   18-JUN-1999; 99US-0139457.
PR   18-JUN-1999; 99US-0139458.
PR   18-JUN-1999; 99US-0139459.
PR   18-JUN-1999; 99US-0139460.
PR   18-JUN-1999; 99US-0139461.
PR   18-JUN-1999; 99US-0139462.
PR   18-JUN-1999; 99US-0139463.
PR   18-JUN-1999; 99US-0139750.
PR   18-JUN-1999; 99US-0139763.
PR   21-JUN-1999; 99US-0139817.
PR   22-JUN-1999; 99US-0139889.
PR   23-JUN-1999; 99US-0140354.
PR   24-JUN-1999; 99US-0140605.
PR   28-JUN-1999; 99US-0140823.
PR   29-JUN-1999; 99US-0140991.
PR   30-JUN-1999; 99US-0141287.
PR   01-JUL-1999; 99US-0141842.
PR   02-JUL-1999; 99US-0142154.
PR   02-JUL-1999; 99US-0142055.
PR   08-JUL-1999; 99US-0142290.
PR   08-JUL-1999; 99US-0142803.
PR   09-JUL-1999; 99US-0142920.
PR   12-JUL-1999; 99US-0142977.
PR   13-JUL-1999; 99US-0143542.
PR   14-JUL-1999; 99US-0143624.
PR   15-JUL-1999; 99US-0144005.
PR   16-JUL-1999; 99US-0144085.
PR   16-JUL-1999; 99US-0144086.
PR   16-JUL-1999; 99US-0144325.
PR   19-JUL-1999; 99US-0144331.
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PR   19-JUL-1999;   99US-0144332.
PR   19-JUL-1999;   99US-0144333.
PR   19-JUL-1999;   99US-0144334.
PR   19-JUL-1999;   99US-0144335.
PR   20-JUL-1999;   99US-0144352.
PR   20-JUL-1999;   99US-0144632.
PR   20-JUL-1999;   99US-0144814.
PR   20-JUL-1999;   99US-0144884.
PR   21-JUL-1999;   99US-0145086.
PR   21-JUL-1999;   99US-0145086.
PR   21-JUL-1999;   99US-0145088.
PR   22-JUL-1999;   99US-0145085.
PR   22-JUL-1999;   99US-0145087.
PR   22-JUL-1999;   99US-0145089.
PR   23-JUL-1999;   99US-0145145.
PR   23-JUL-1999;   99US-0145192.
PR   23-JUL-1999;   99US-0145218.
PR   23-JUL-1999;   99US-0145224.
PR   26-JUL-1999;   99US-0145276.
PR   27-JUL-1999;   99US-0145913.
PR   27-JUL-1999;   99US-0145918.
PR   27-JUL-1999;   99US-0145919.
PR   28-JUL-1999;   99US-0145951.
PR   02-AUG-1999;   99US-0146386.
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PR   04-AUG-1999;   99US-0147204.
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PR   05-AUG-1999;   99US-0147192.
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PR   06-AUG-1999;   99US-0147303.
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PR   10-AUG-1999;   99US-0148171.
PR   11-AUG-1999;   99US-0148319.
PR   12-AUG-1999;   99US-0148341.
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PR   13-AUG-1999;   99US-0148684.
PR   16-AUG-1999;   99US-0149368.
PR   17-AUG-1999;   99US-0149175.
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PR   23-AUG-1999;   99US-0149902.
PR   23-AUG-1999;   99US-0149930.
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PR   26-AUG-1999;   99US-0150884.
PR   27-AUG-1999;   99US-0151065.
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PR   27-AUG-1999;   99US-0151080.
PR   30-AUG-1999;   99US-0151303.
PR   31-AUG-1999;   99US-0151438.
PR   01-SEP-1999;   99US-0151930.
PR   07-SEP-1999;   99US-0152363.
PR   10-SEP-1999;   99US-0153070.
PR   13-SEP-1999;   99US-0153758.
PR   15-SEP-1999;   99US-0154018.
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PR   05-OCT-1999;   99US-0157753.
PR   05-OCT-1999;   99US-0157865.
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PR   07-OCT-1999;   99US-0158029.
PR   08-OCT-1999;   99US-0158232.
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PR   14-OCT-1999;   99US-0159331.
PR   14-OCT-1999;   99US-0159637.
PR   14-OCT-1999;   99US-0159638.
PR   18-OCT-1999;   99US-0159584.
PR   21-OCT-1999;   99US-0160741.
PR   21-OCT-1999;   99US-0160767.
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PR   21-OCT-1999;   99US-0160770.
PR   21-OCT-1999;   99US-0160815.
PR   22-OCT-1999;   99US-0160980.
PR   22-OCT-1999;   99US-0160981.
PR   22-OCT-1999;   99US-0160989.
PR   25-OCT-1999;   99US-0161404.
PR   25-OCT-1999;   99US-0161405.
PR   25-OCT-1999;   99US-0161406.
PR   26-OCT-1999;   99US-0161359.
PR   26-OCT-1999;   99US-0161360.
PR   26-OCT-1999;   99US-0161361.
PR   28-OCT-1999;   99US-0161920.
PR   28-OCT-1999;   99US-0161992.
PR   28-OCT-1999;   99US-0161993.
PR   29-OCT-1999;   99US-0162142.
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Query Match               6.5%;  Score 193;  DB 21;  Length 348;
Best Local Similarity   27.1%;  Pred. No. 5.6e-08;  Indels 16;  Gaps 7;
Matches   61;  Conservative   57;  Mismatches   91;

Qy   352  SYLRLRERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLG  411
               :||| | |::|  |: :  :   :: ::| | |:||      :::
Db    80  ayiremegkpkhrplpd---ylekv-qsdltphmravlvdwlvevaeeyklvsdtlylt  134

Qy   412  VGLLDRFLSKGSFKSERTLILVGIASLTLATRIEENQPYNSIRKRNFT-IQNLRYSRHEV  470
            : :|||| | |||:|||:  :::|:|  |::| |||    |  |  ||  ||
Db   135  isyvdrflsvkpinrqk-lqlvgvsamliaskyeeigp---pkvedfcyitdntftkgev  190

Qy   471  VAMEWLVQEVLNRKCFTPFIFNFLWFYLKAAR------ANPEVERKAKSLAVTSLSDQTQL  525
            |:|  :| |||  :| ||  |:  ||   :      || ||
Db   191  vsmeadillalqfelgsptiktflrrifrvaqedfkdsqlqieflccylselsmldytcv  250

Qy   526  CFWPSTVAAALVVLA-CIEHNKISAYQRVIKVHVRTTDNELPECV  569
            |:|| ||   : |||           || |  ||
Db   251  kylpsllsasavflarflirfllrpkghpwnqmleeytkykaadlqycv  295


RESULT 13
AAG24670
ID   AAG24670 standard; Protein; 360 AA.
XX
AC   AAG24670;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 28435.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000;  2000EP-0301439.
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PR   25-FEB-1999;  99US-0121825.
PR   05-MAR-1999;  99US-0123180.
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AC   AAG24669;
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DT   17-OCT-2000 (first entry)
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KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.

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Db   92 aylremegkphrplpd---ylekv-qsdltphmravivdwlvevaeeyklvsdtlylt 146

Qy  412 VGLLDRFLSKGSFFKSERTLILVGIASLTLATRIEENQPYNSIRKRNFT-IQNLRYSRHEV 470
            |:||||  |    | |:||  :|  |: ||| |:  :|  ::  |  ||  :|
Db  147 lsydvrlskpinrqk-lqlvgvsamllaskyeeigp---pkvedfcyitdntftkqev 202

Qy  471 VAMEWLVQEVLNFKCFTPTINFLWFYLKAAR----ANPEVERKAKSLAVTSLSDQTQL 525
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Db  203 vsmeadllalqfelgsptiktflirfrtrvaqedfkdsqlqeflccylseismldytcv 262

Qy  526 CFWPSTVAAALVVLA-CIEHNKISAYQRVIKVHVRTTDNELPCV 569
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Query Match   6.5%;   Score 193;   DB 21;   Length 369;
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Qy   412 VGLLDRFLSKGSSFKSERTLILVGIASTLATRIEENQPYNSIRKRNFT-TQNLRYSRHEV 470
         :|||| | || :|||:|||||::::| |||::||:|| ::| | |::| ||
Db   156 isyvdrflsvkplnrqk-lqlvgvsamliaskyeeigp--pkvedfcyitdntfkqev 211

Qy   471 VAMEWLVQEVLNFKCFTPTIFNFLWFYIKAAR------ANPEVERKAKSLAVTSLSDQTQL 525
         |:| :||| |:| ::| |::| | |:: ||::| |:|:|| | ::|
Db   212 vsmeadillalqfelqspttktflrrttrvaqedfkdsqlqeflccylselsmldytcv 271

Qy   526 CFWPSTVAAALVVLA-CIEHNKISAYQRVIKVHVHRTTDNELPECV 569
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Db   272 kylpsllsasavflarfiirpkqhpwnqmleeytkykaadlqvcv 316

RESULT 15
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AC   AAW00365;
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DT   24-JAN-1997 (first entry)
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KW   Cyclin B1; cell cycle regulatory protein; CCRP; inhibitor;
KW   apoptosis; cell differentiation.
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OS   Homo sapiens.

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PN    WO9633286-A1.
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PD    24-OCT-1996.
XX
PF    19-APR-1996;   96WO-US05643.
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PR    20-APR-1995;   95US-0425299.
XX
PA    (HARD ) HARVARD COLLEGE.
XX
PI    King RW,  Kirschner MW,  Peters J;
XX
DR    WPI; 1996-485790/48.
DR    N-PSDB; AAT41775.
XX
PS    Sequence  433 AA;
XX
CC    Human cyclin B1 (AAW00365) was expressed as a GST-cyclin B1 fusion
CC    protein, utilising cDNA (see also AAT41775) amplified by PCR and
CC    vector pGEX-4T-2.  Cyclin B1 can be used in a novel ubiquitin-
CC    conjugating system, together with e.g. ubiquitin-activating enzyme
CC    (see also AAW00362), ubiquitin-conjugating enzyme (AAW00363), a
CC    mitotic destruction complex comprising CDC27 (AAW00364) and
CC    biotinylated ubiquitin, to identify inhibitors of ubiquitin-
CC    mediated proteolysis of cell cycle regulatory proteins.
XX
PT    Detecting inhibitors of ubiquitin-mediated proteolysis of CCRPs -
PT    used in the treatment of proliferative and/or differentiation
PT    diseases, and in modulation of apoptosis
XX
PS    Example 1; Page 41-42; 63pp; English.
XX
SQ    Sequence  433 AA;

Query Match             6.5%;   Score 191;  DB 17;  Length 433;
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Qy    170 HVSNSRSLNFESENKESDVVSVIS--GVEYCSKFGSVTGGADNEEIEISKPSSFVEADSS 227
              || |    :| : : :|||:           :::    :|   |||| ||: : :::  ::|
Db     12 naenkakinnagakrvptapaatskpglrprtalgdi-gnkvseqlqakmpmkkeakpsa 70

Qy    228 LGSA--KELKPELEIYGCVSDLACSERKFSEEVSDSLDDESSEQRSEIYSQYSDFDYSDYT 285
              ||||    | | : :     |  ||   :| :| | ||:                    ::
Db     71 tgkvidkklpkplekvpmlvpvpvsepvpepepepepvkeek-----------ls 116

Qy    286 PS-IFFDSGSEFSEKSSSDSPISHSRSLYLQFKEQFCRS-----TIPNDFGSSCEEEIHS 339
              |:  |          |   :| : ||                        :| ::
Db    117 pepilvdtaspspmetsgcapa-----------eedlcqafsdvilavndv--daedgadp 164

Qy    340 ELLRFDDEEVEESYLRLRERERSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCS 399
              |||:  |     : :  |:    : ::||          |     :| | |   ::|  |
Db    165 nlc-----seyvkdiyaylrqleeqa-----vrpkyligrevtg---nmralildwlvqvqm 214

Qy    400 DMGLQQETLFLGVGLLDRFLSKGSFKSERTLILVGIASLTLATRIEENQPYNSIRKRNFT 459
              | :  : | : : ||:  || ::| : :: |  :| |||| || ||:  | ||:| |
Db    215 kfrllqetmyntvsiidrfm-qnncvpkkmlqlvgvtamfiaskyeemyp-peigdfafv 272

Qy    460 IQNLRYSRHEVVAMEWLVQEVLNFKCGFTPTIPNFLWFYLKAARANPEVERKAKSLAVTSL 519
              | ||:  |  ::||:    || |: |  || |  | || :  | : |  ||: | : :|
Db    273 tdn-tytkhqirqmemkilralnfglgrplplhflrraskigevdveghtlakylmelti 331

Qy    520 SDQTQLCFWPSTVAALVVLA 540
              :  | | | |:|| | ||:
Db    332 ldydmvhfppsqiaagafcla 352
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Search completed: July 23, 2002, 14:22:01
Job time: 231 sec